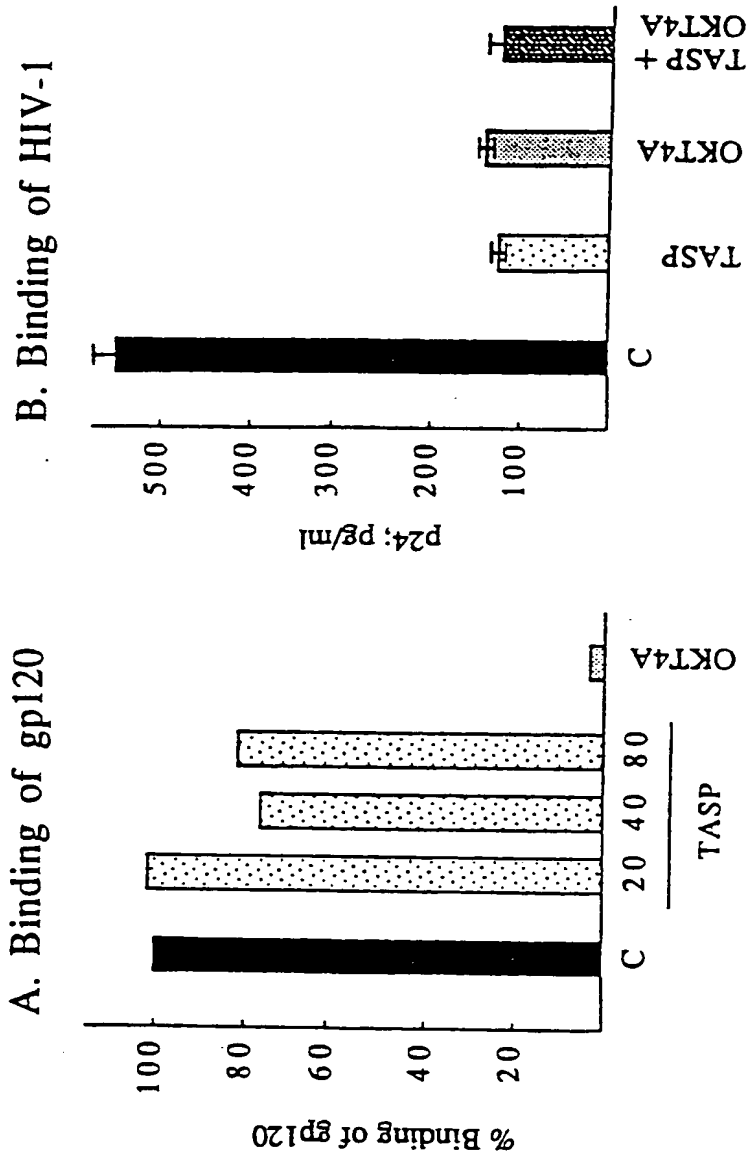

A. Binding of gp120
% Binding of gp120
100
80
60
40
20
C
20
40
80
TASP
OKT4A
B. Binding of HIV-1
p24: pg/ml
500
400
300
200
100
C
TASP
OKT4A
TASP +
OKT4A

FIGURE 1

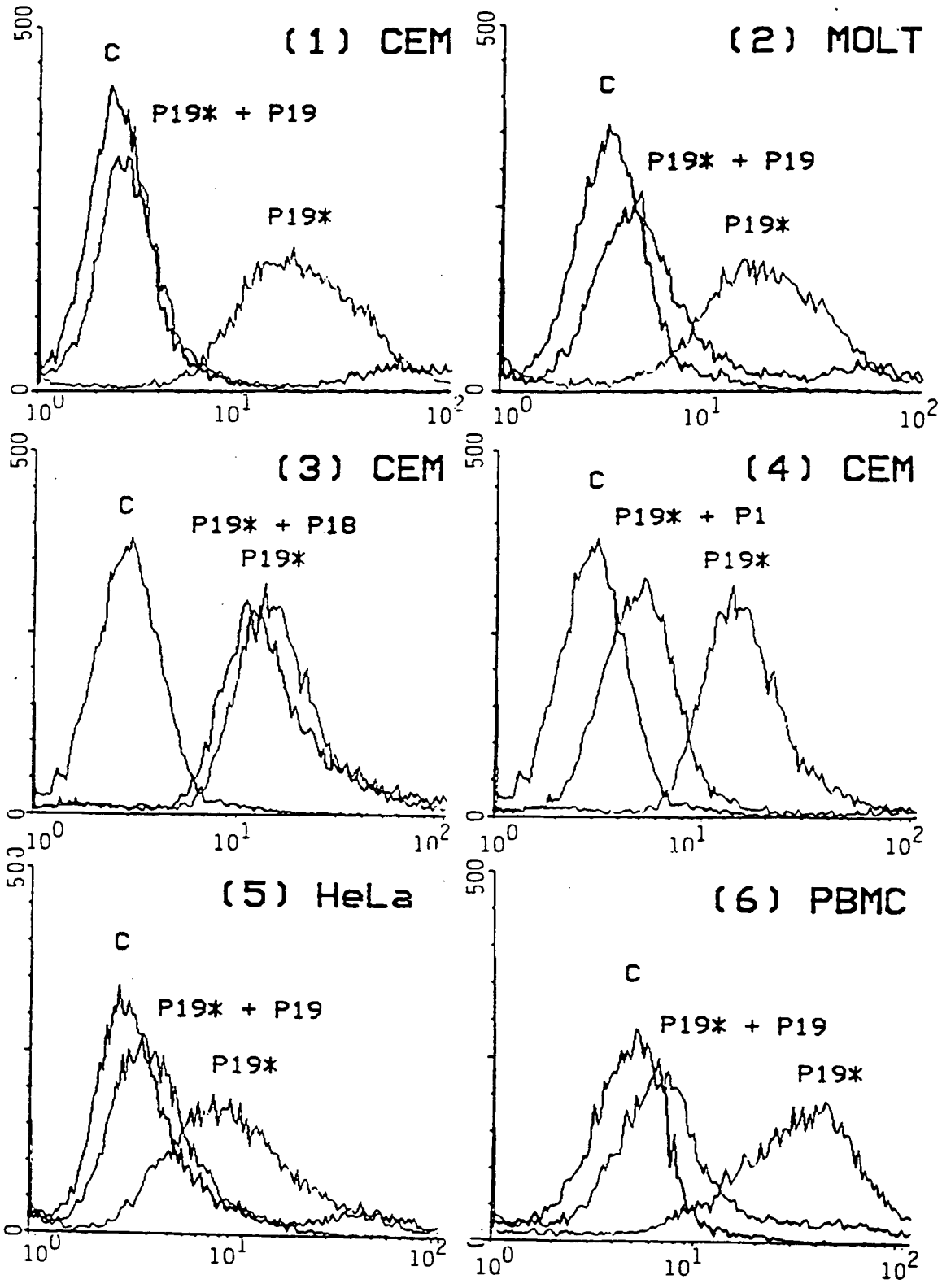

(1) CEM
C
P19* + P19
P19*
(2) MOLT
C
P19* + P19
P19*
(3) CEM
C
P19* + P18
P19*
(4) CEM
C
P19* + P1
P19*
(5) HeLa
C
P19* + P19
P19*
(6) PBMC
C
P19* + P19
P19*
500
0
10^0
10^1
10^2

FIGURE 2

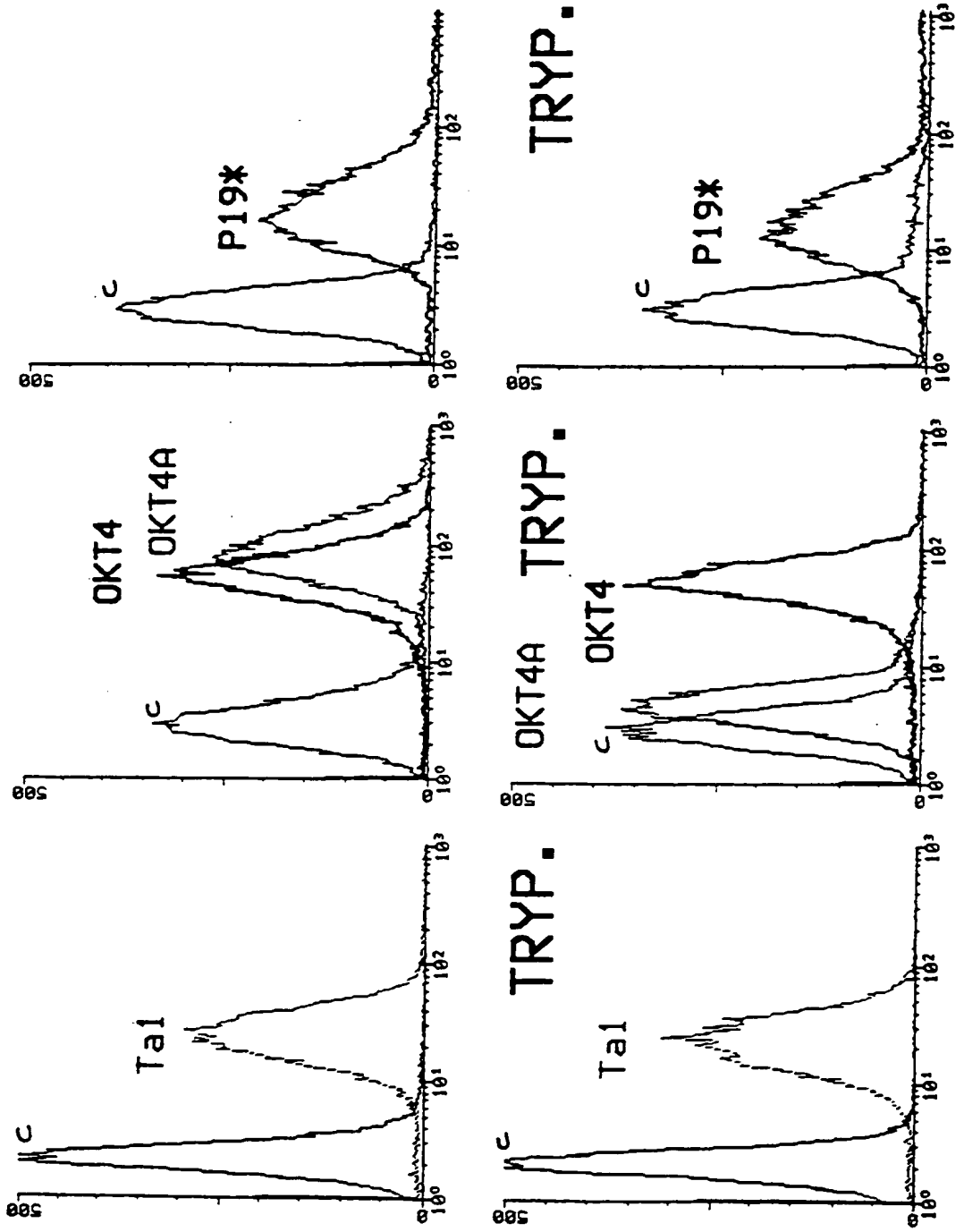

SELECTED PREFERENCES:
Tal
TRYP.
OKT4
OKT4A
OKT4A
OKT4
P19*
P19*
C
500
0
10^0
10^1
10^2
10^3

FIGURE 3A

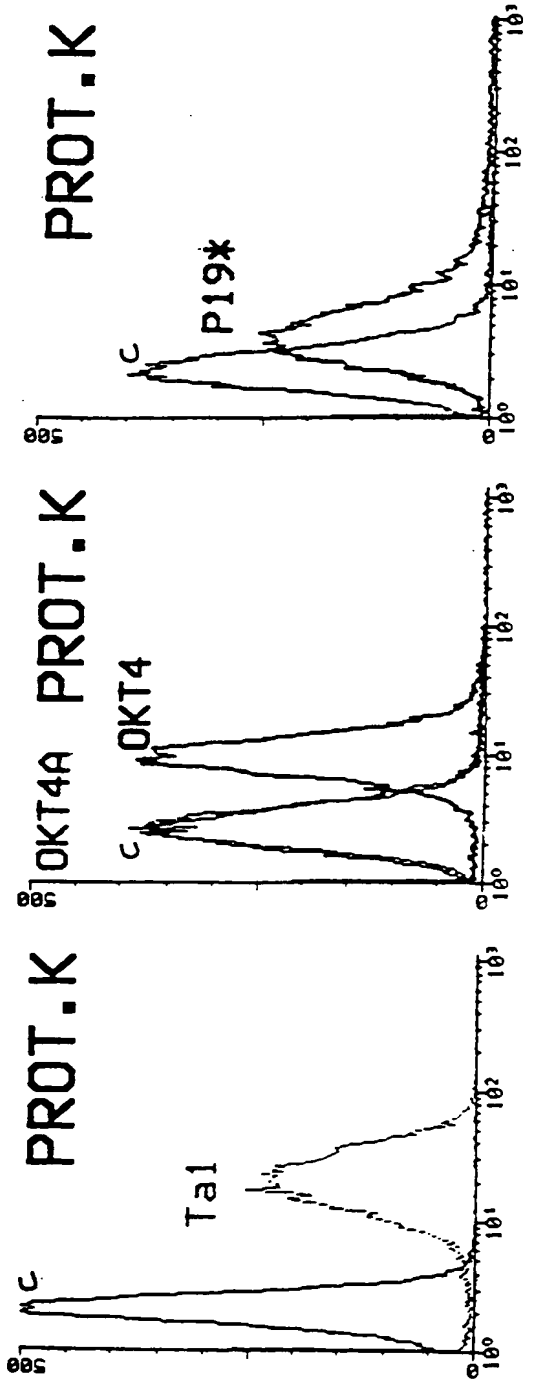


FIGURE 3B

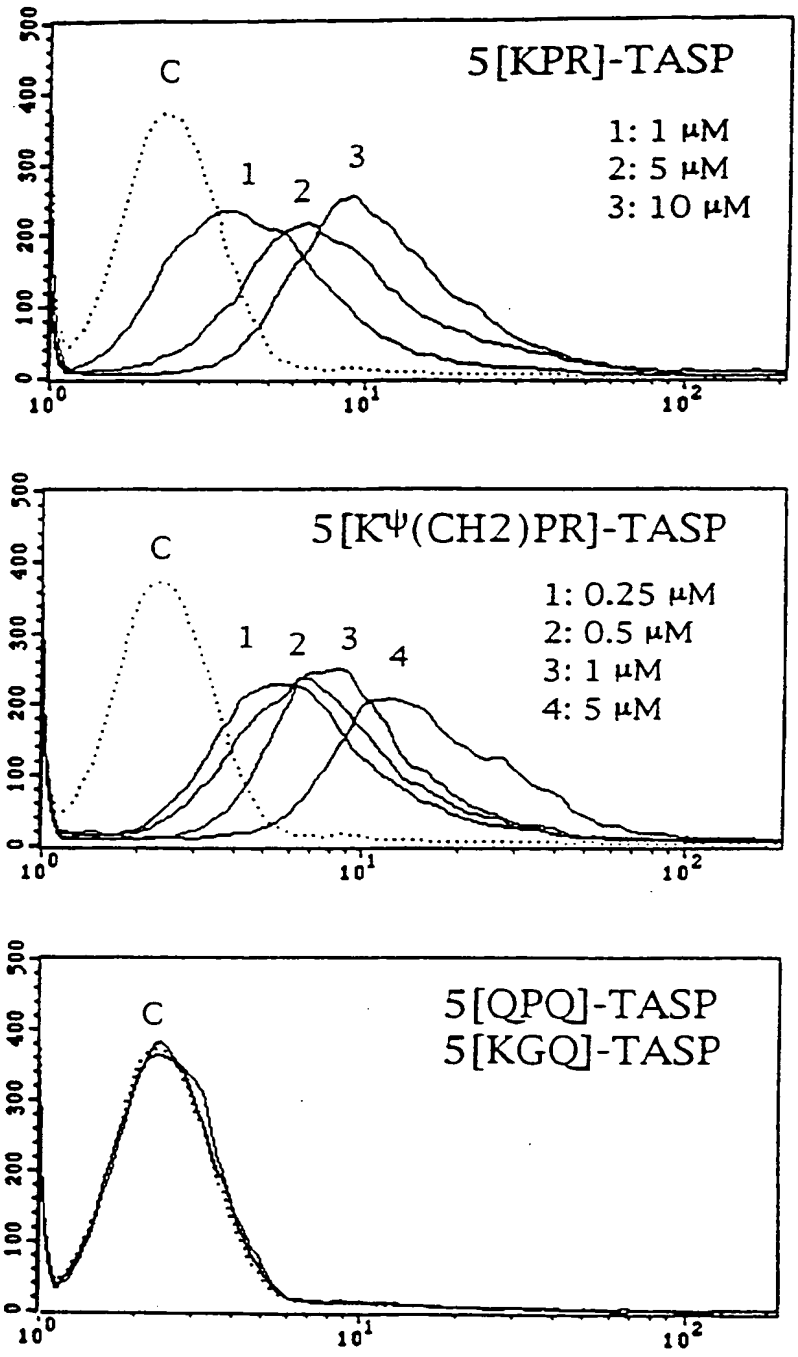

5[KPR]-TASP
C
1
2
3
1: 1 µM
2: 5 µM
3: 10 µM
5[KΨ(CH2)PR]-TASP
C
1
2
3
4
1: 0.25 µM
2: 0.5 µM
3: 1 µM
4: 5 µM
5[QPQ]-TASP
5[KGQ]-TASP
C
0
100
200
300
400
500
10^0
10^1
10^2

FIGURE 4

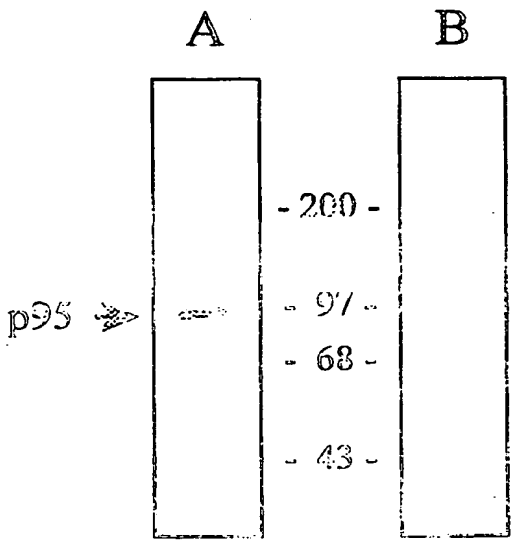


FIGURE 5

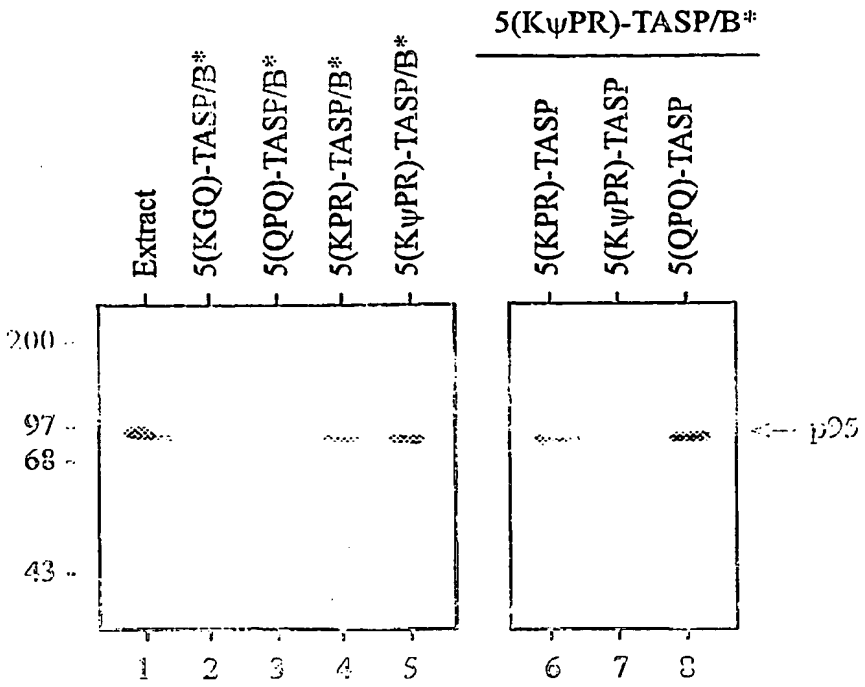


FIGURE 6

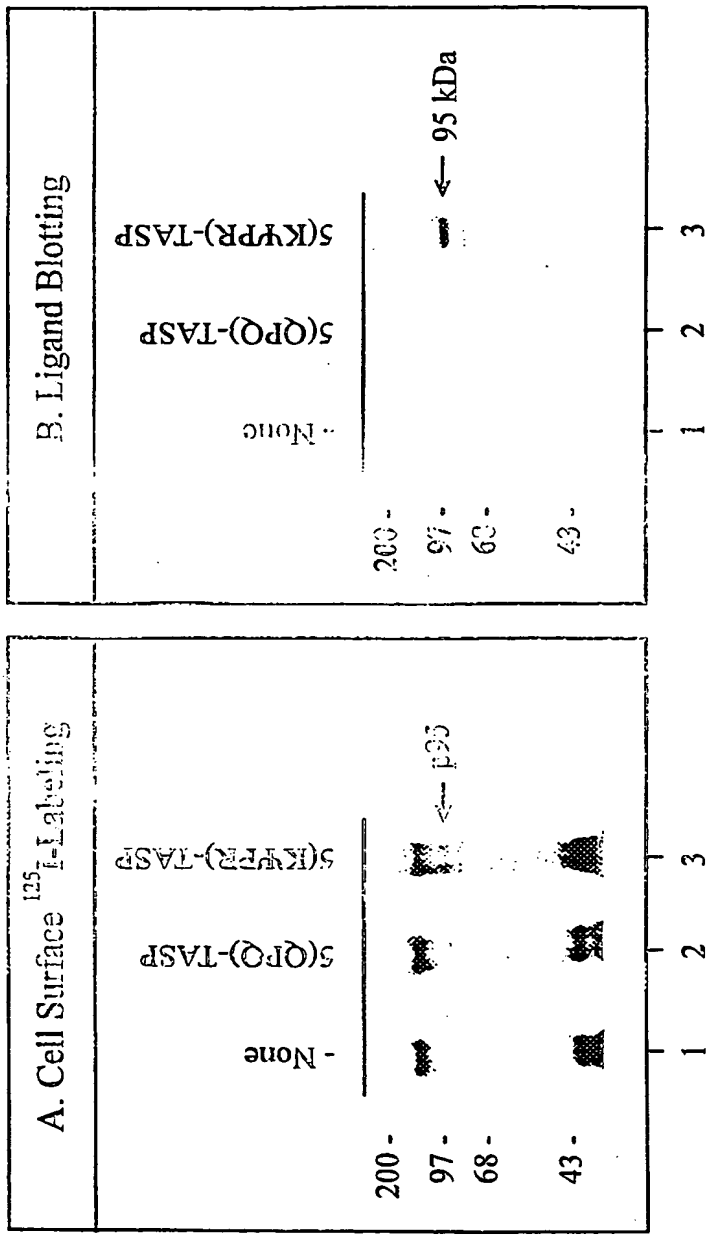


FIGURE 7

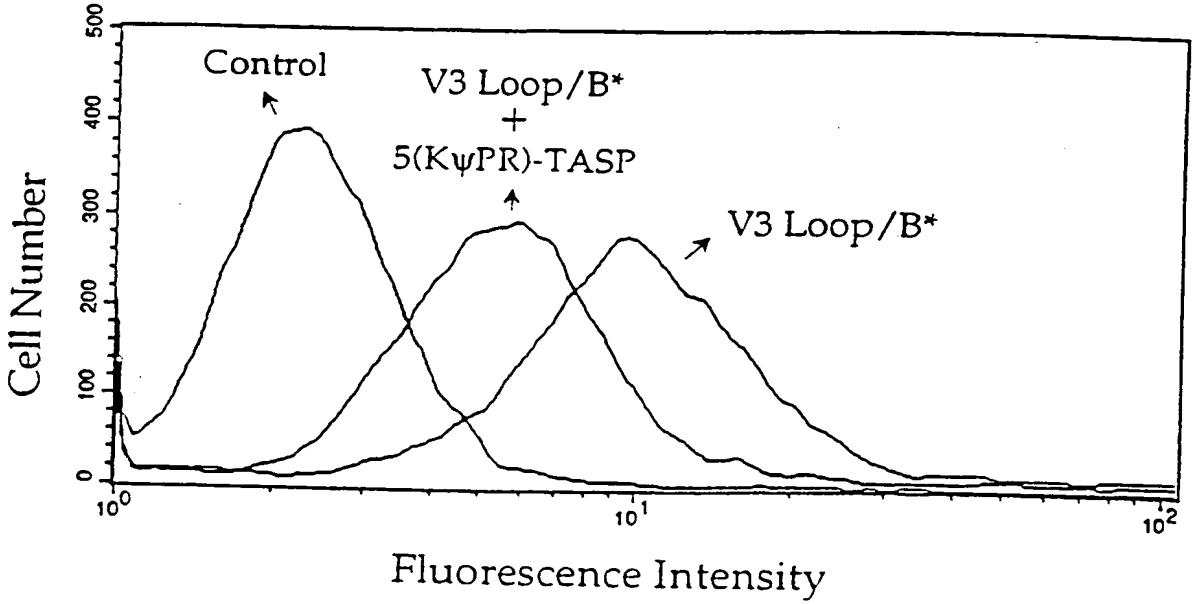

Control
V3 Loop/B*
+
5(KψPR)-TASP
V3 Loop/B*
Cell Number
0
100
200
300
400
500
10^0
10^1
10^2
Fluorescence Intensity

FIGURE 8A

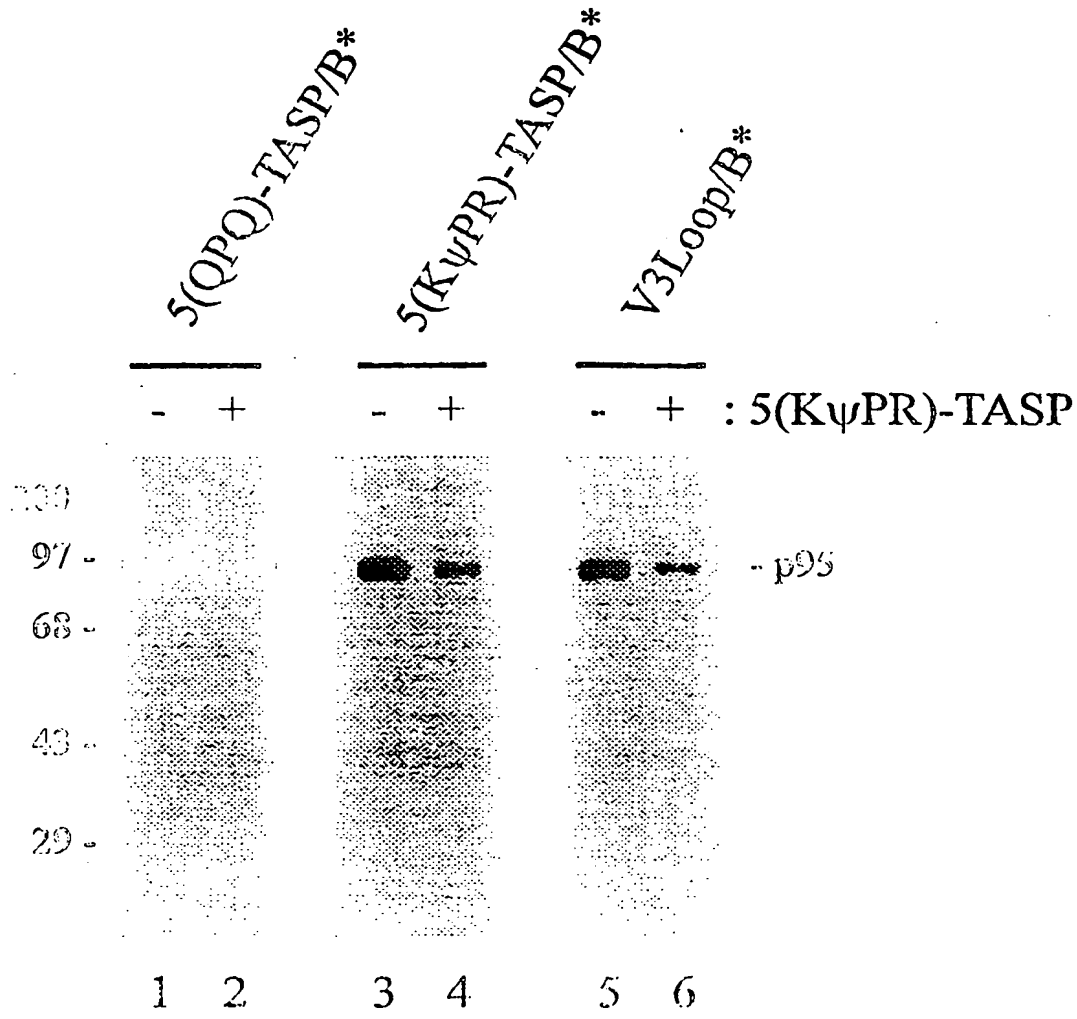

5(QPQ)-TASP/B*
5(KψPR)-TASP/B*
V3Loop/B*
- + - + - + : 5(KψPR)-TASP
97 -
68 -
43 -
29 -
- p95
1 2 3 4 5 6

FIGURE 8B

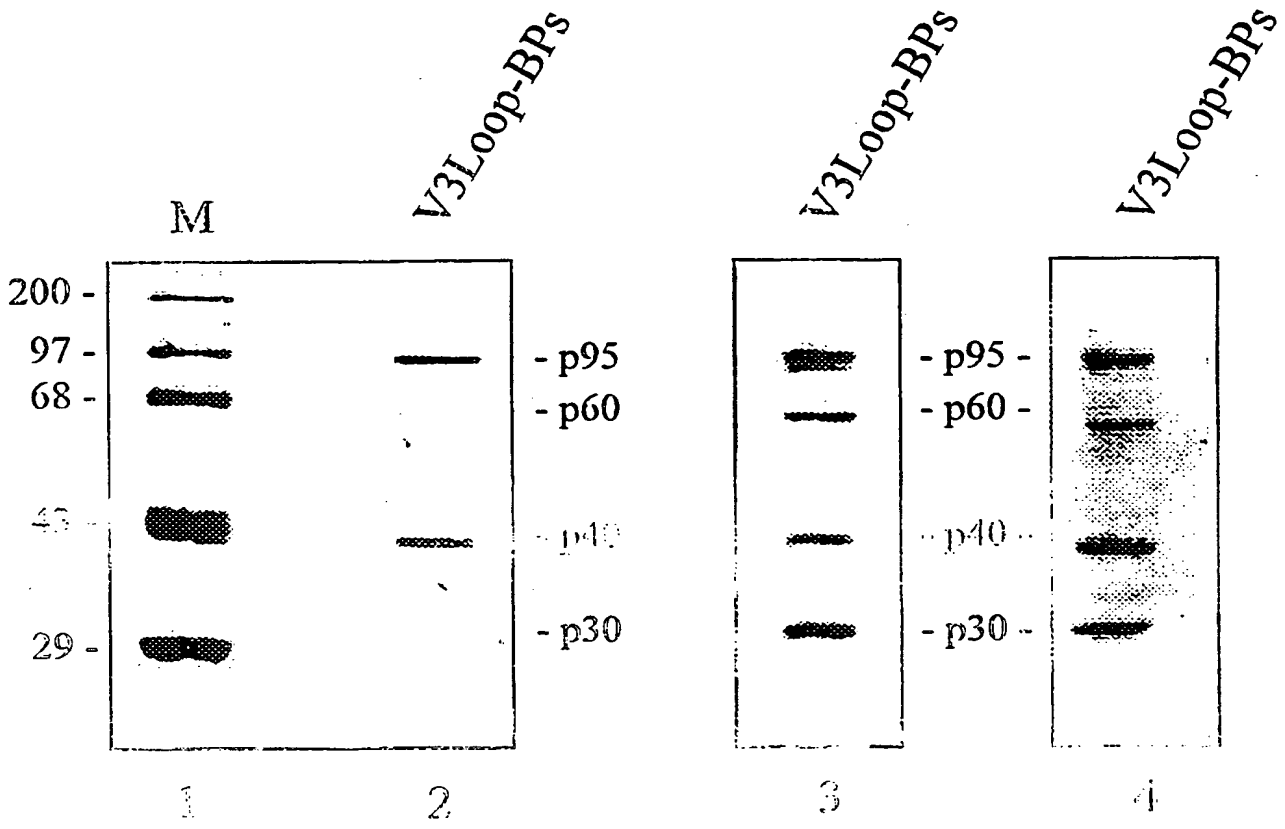

M
V3Loop-BPs
V3Loop-BPs
V3Loop-BPs
200 -
97 -
68 -
43 -
29 -
- p95
- p60
- p40
- p30
- p95 -
- p60 -
- p40 -
- p30 -
1
2
3
4

FIGURE 9

FIGURE 10

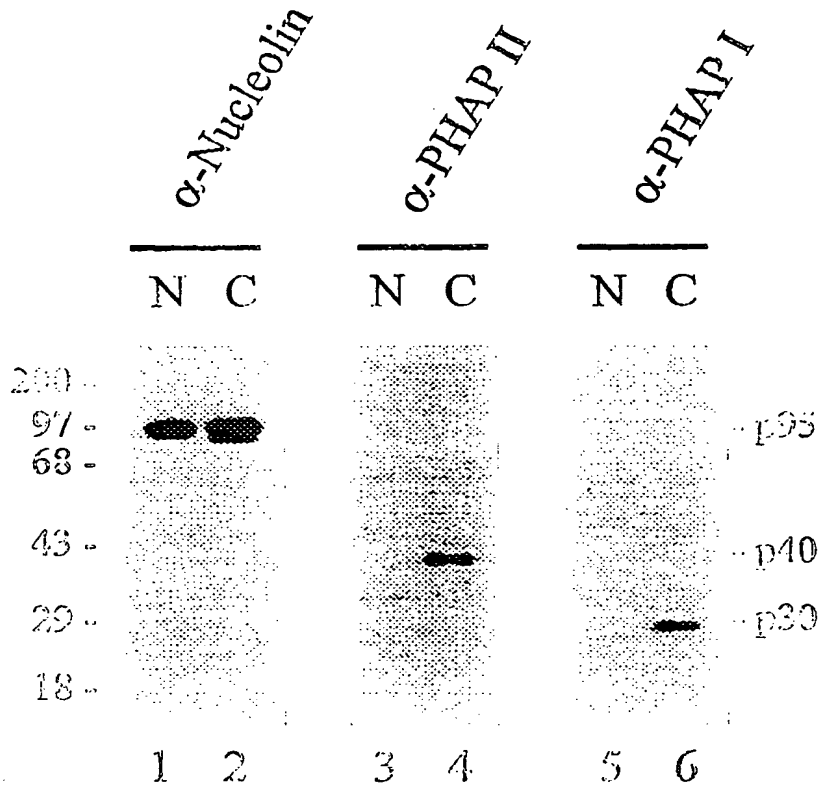


FIGURE 11

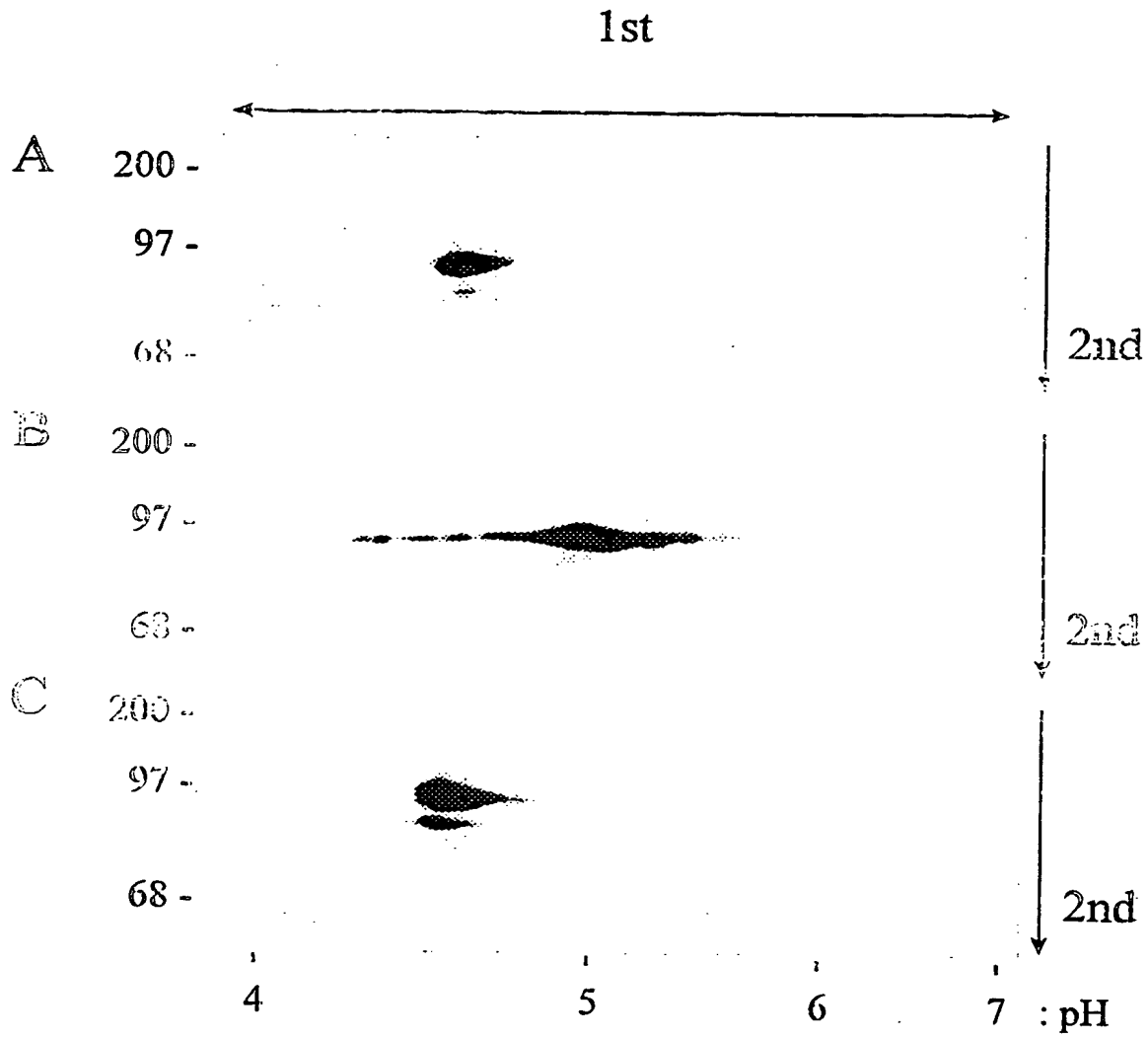


FIGURE 12

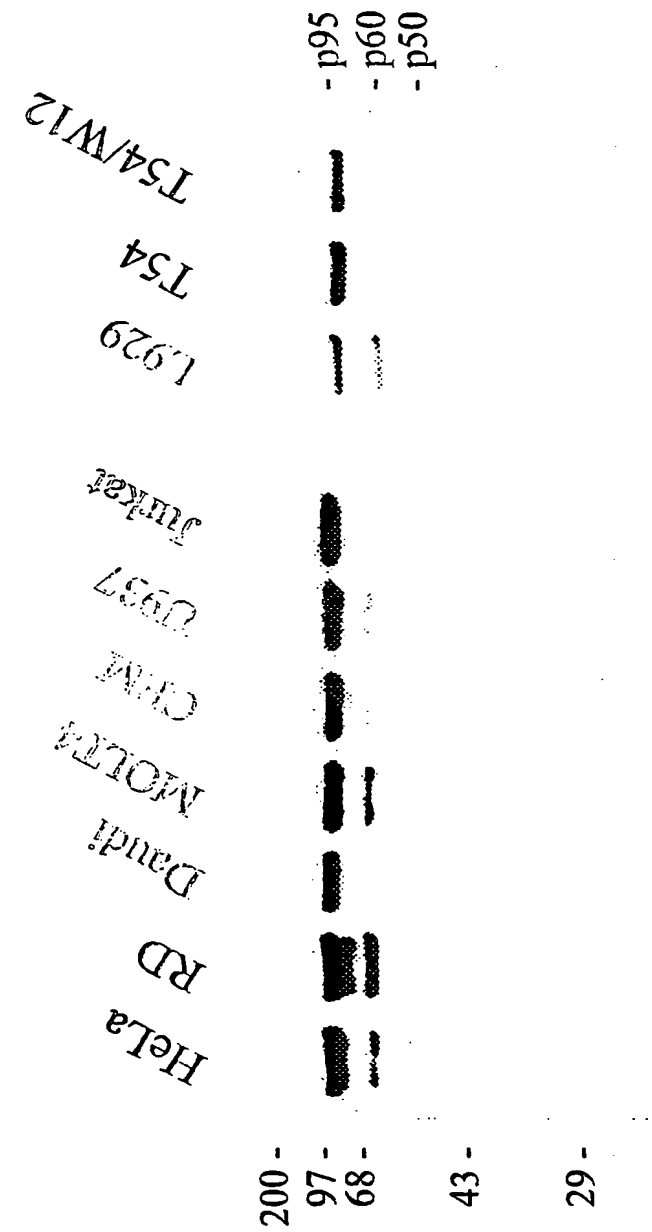

200 -
97 -
68 -
43 -
29 -
- p95
- p60
- p50
HeLa
RD
Daudi
MOLT4
CEM
Jurkat
L929
T54
T54/W12

FIGURE 13A

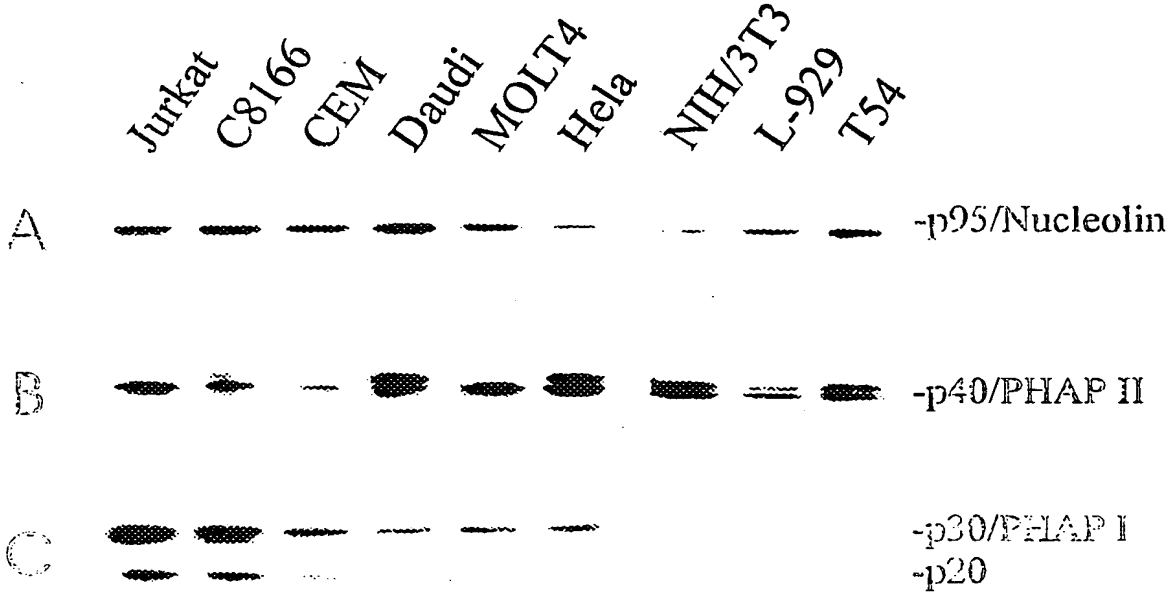
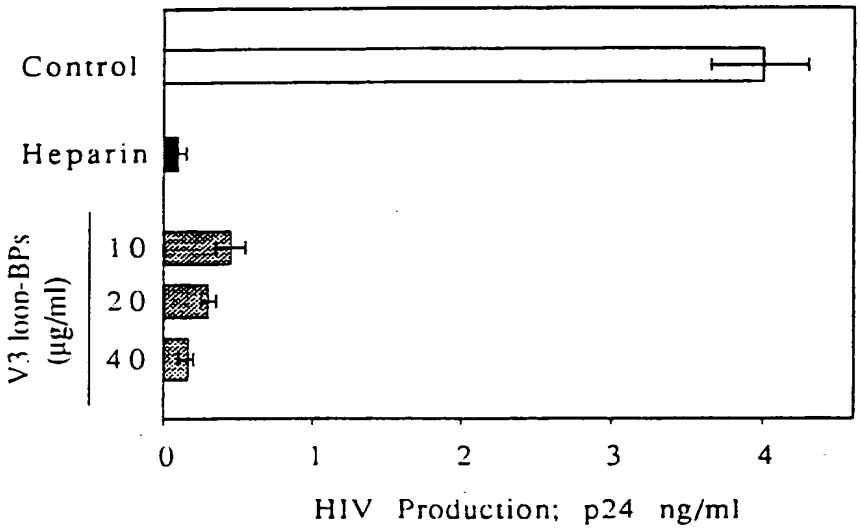

Jurkat
C8166
CEM
Daudi
MOLT4
Hela
NIH/3T3
L-929
T54
A
B
C
-p95/Nucleolin
-p40/PHAP II
-p30/PHAP I
-p20

FIGURE 13B

A.


Control
Heparin
V3 loop-BPs (µg/ml)
10
20
40
0
1
2
3
4
HIV Production; p24 ng/ml

B.

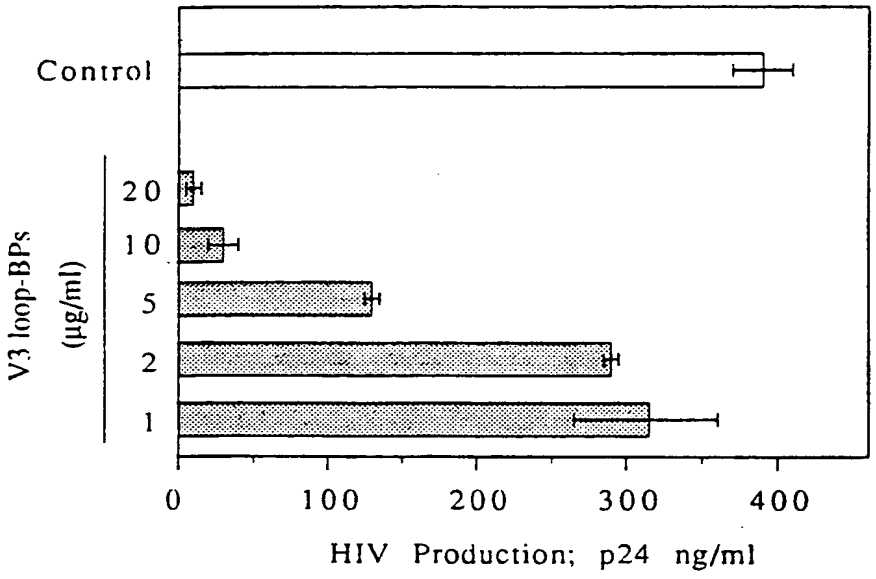

Control
V3 loop-BPs (µg/ml)
20
10
5
2
1
0
100
200
300
400
HIV Production; p24 ng/ml

FIGURE 14

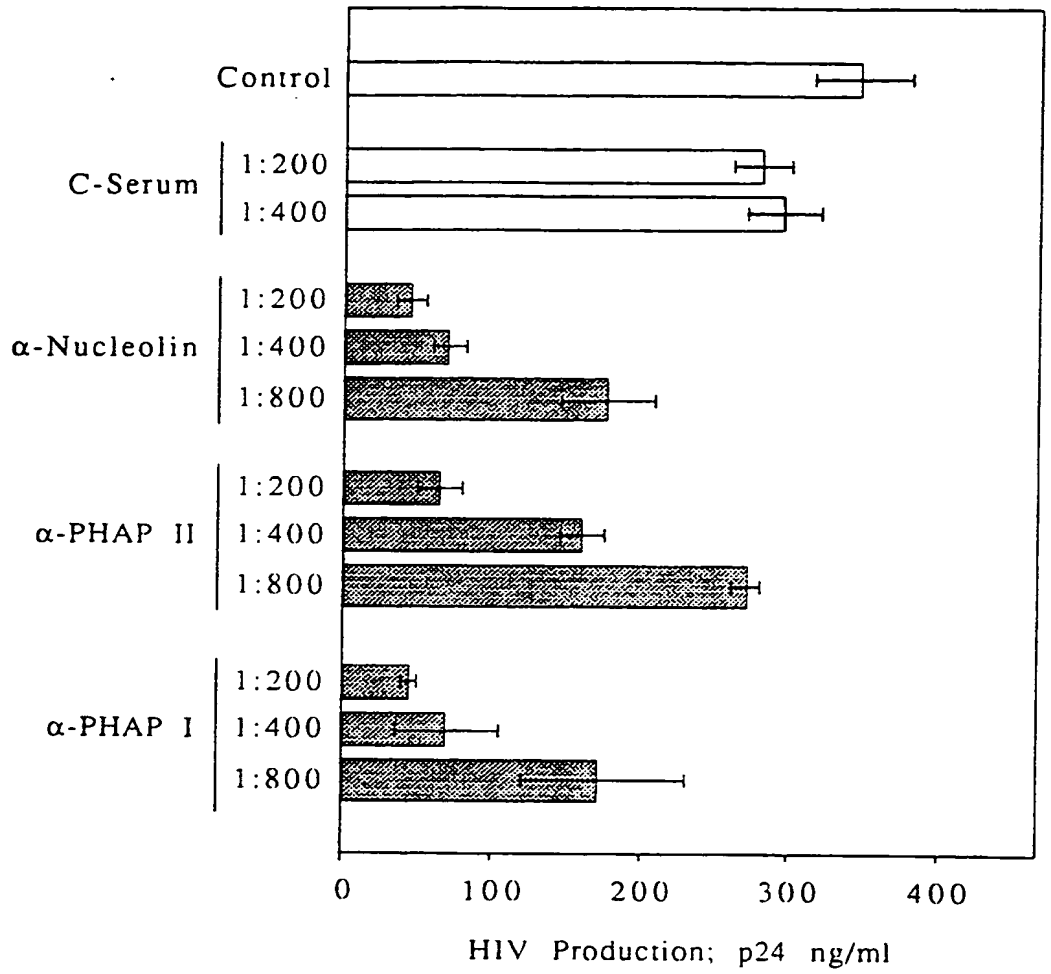
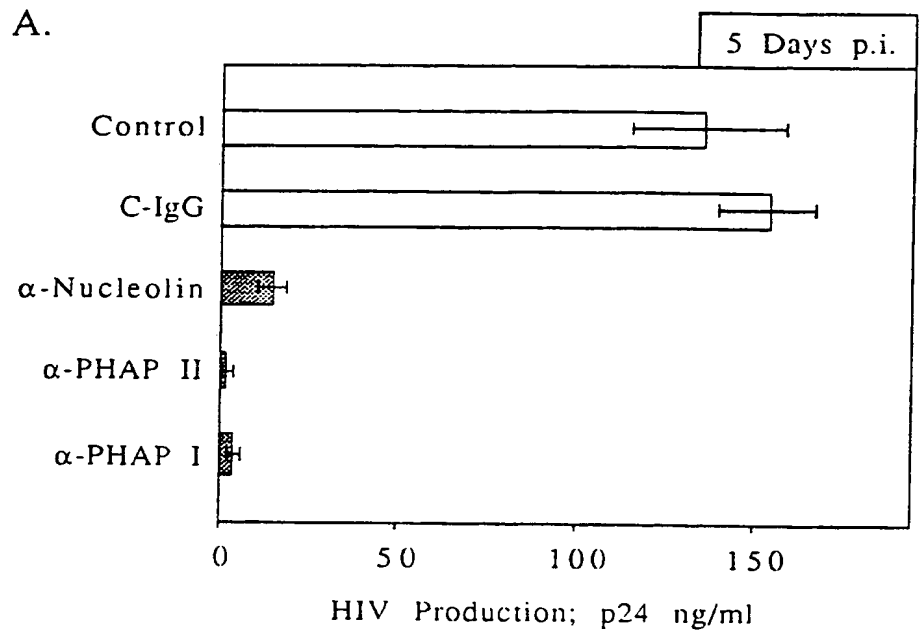

Control
C-Serum
1:200
1:400
α-Nucleolin
1:200
1:400
1:800
α-PHAP II
1:200
1:400
1:800
α-PHAP I
1:200
1:400
1:800
0
100
200
300
400
HIV Production; p24 ng/ml

FIGURE 15


A.
5 Days p.i.
Control
C-IgG
α-Nucleolin
α-PHAP II
α-PHAP I
0
50
100
150
HIV Production; p24 ng/ml

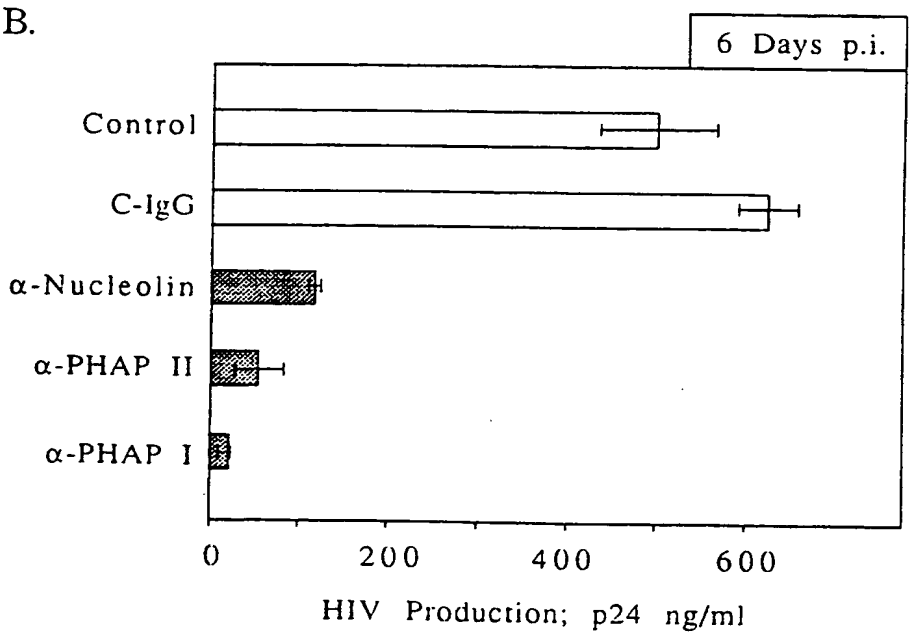

B.
6 Days p.i.
Control
C-IgG
α-Nucleolin
α-PHAP II
α-PHAP I
0
200
400
600
HIV Production; p24 ng/ml

FIGURE 16

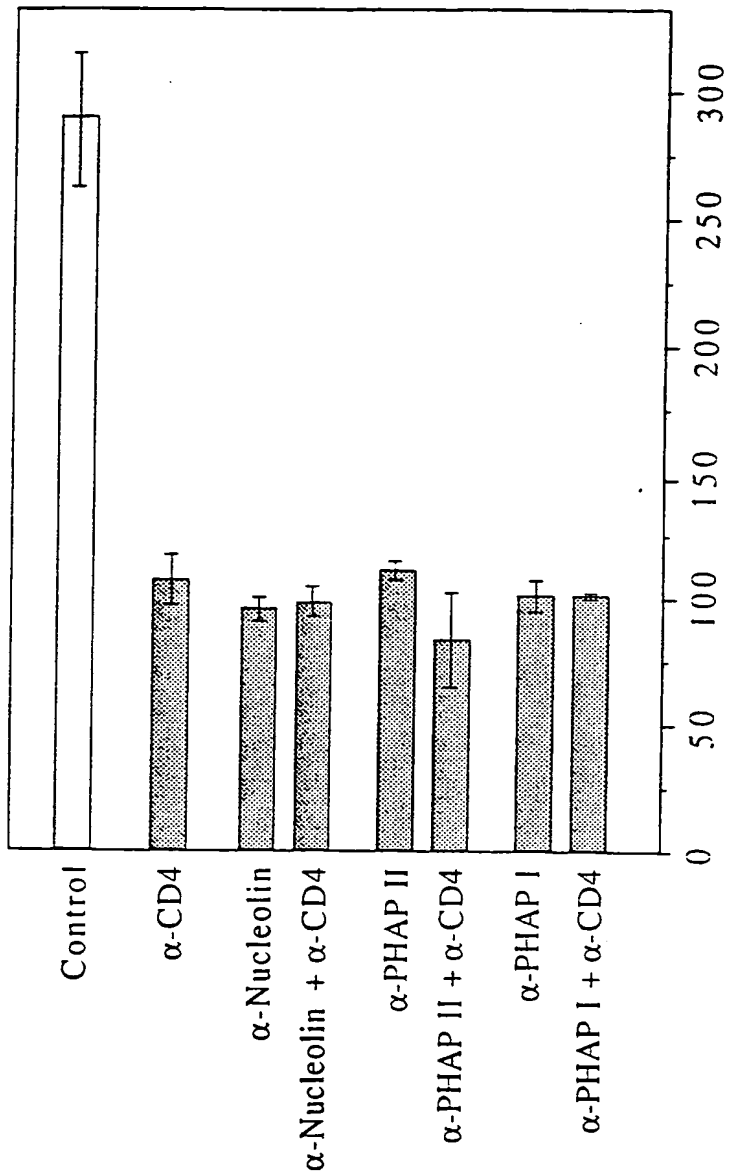

Control
α-CD4
α-Nucleolin
α-Nucleolin + α-CD4
α-PHAP II
α-PHAP II + α-CD4
α-PHAP I
α-PHAP I + α-CD4
0
50
100
150
200
250
300
HIV Binding; p24 pg/ml

FIGURE 17

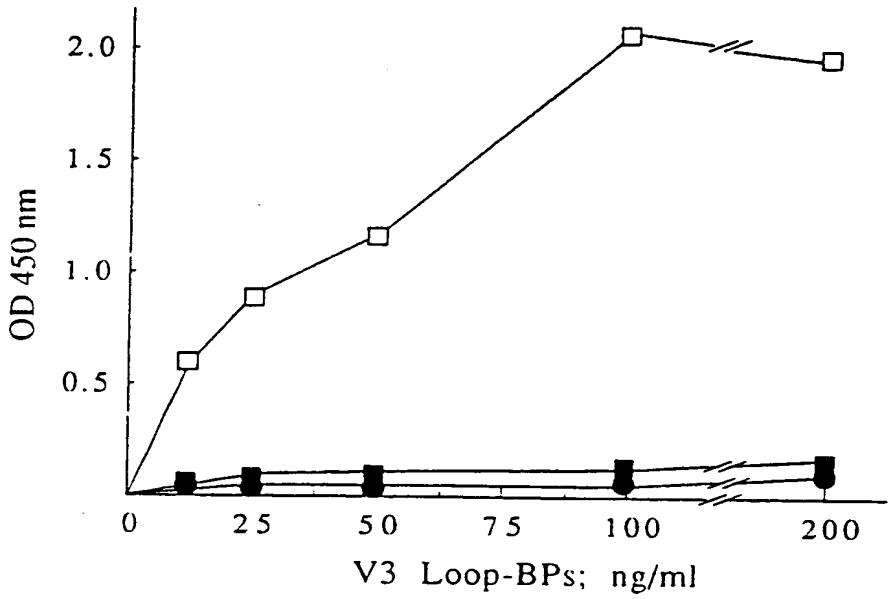
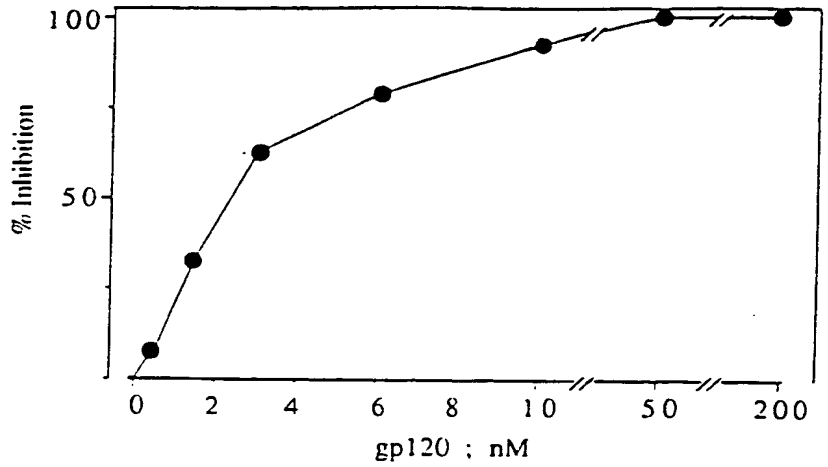
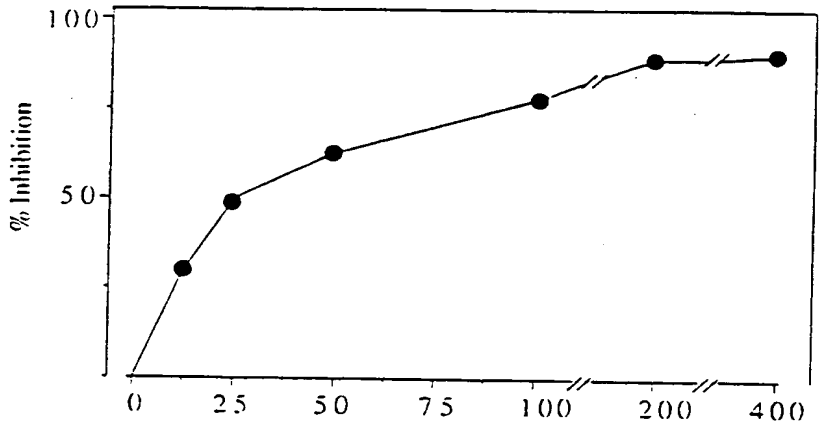


FIGURE 18

A. 5[Kψ(CH2N)PR]-TASP Binding to the V3 loop-BPs



B. gp120 Binding to the V3 loop-BPs



C. gp120 Binding to the V3 loop-BPs

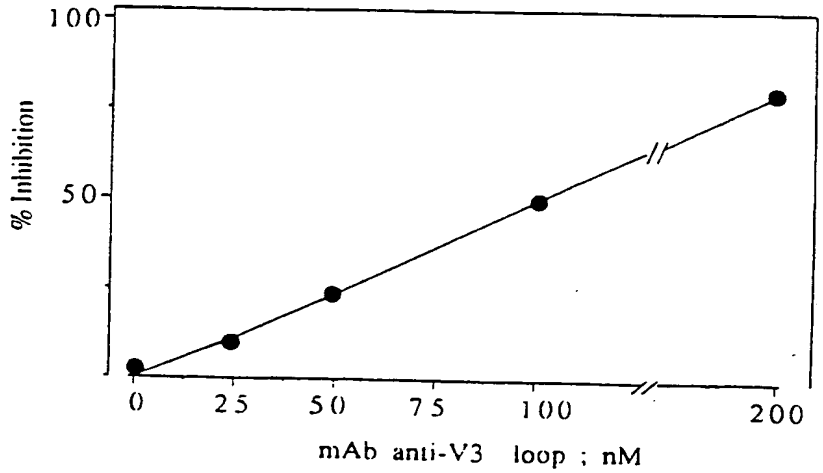


FIGURE 19

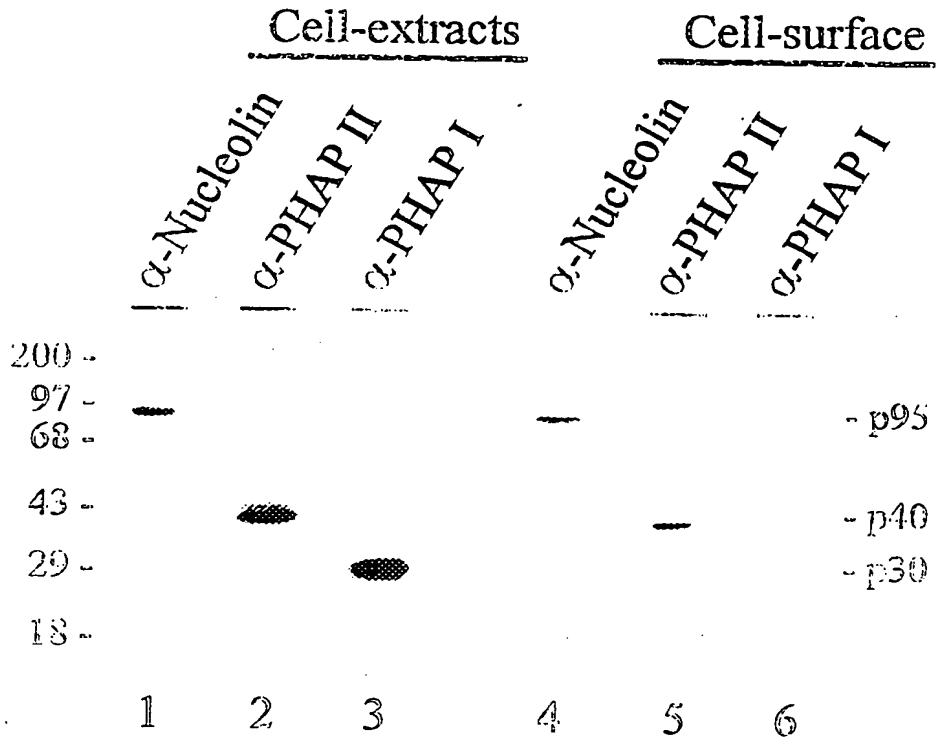

Cell-extracts
Cell-surface
α-Nucleolin
α-PHAP II
α-PHAP I
α-Nucleolin
α-PHAP II
α-PHAP I
200 -
97 -
68 -
43 -
29 -
18 -
- p95
- p40
- p30
1
2
3
4
5
6

FIGURE 20

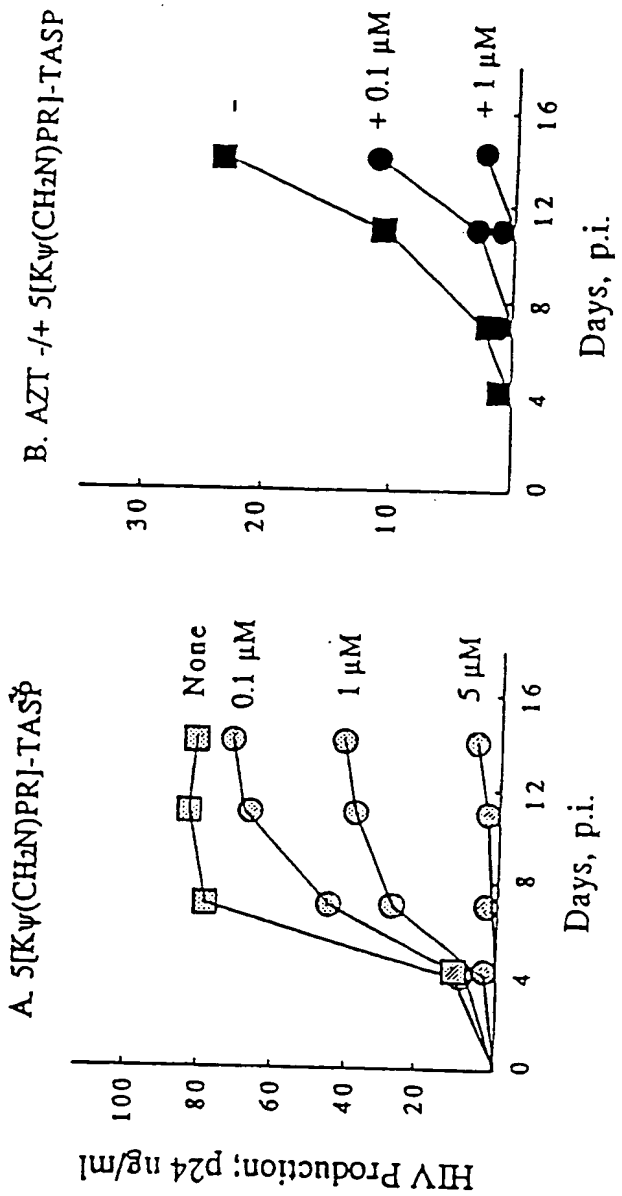

HIV Production; p24 ng/ml
A. 5[Kψ(CH2N)PR]-TASP
None
0.1 µM
1 µM
5 µM
Days, p.i.
B. AZT -/+ 5[Kψ(CH2N)PR]-TASP
-
+ 0.1 µM
+ 1 µM
Days, p.i.

FIGURE 21

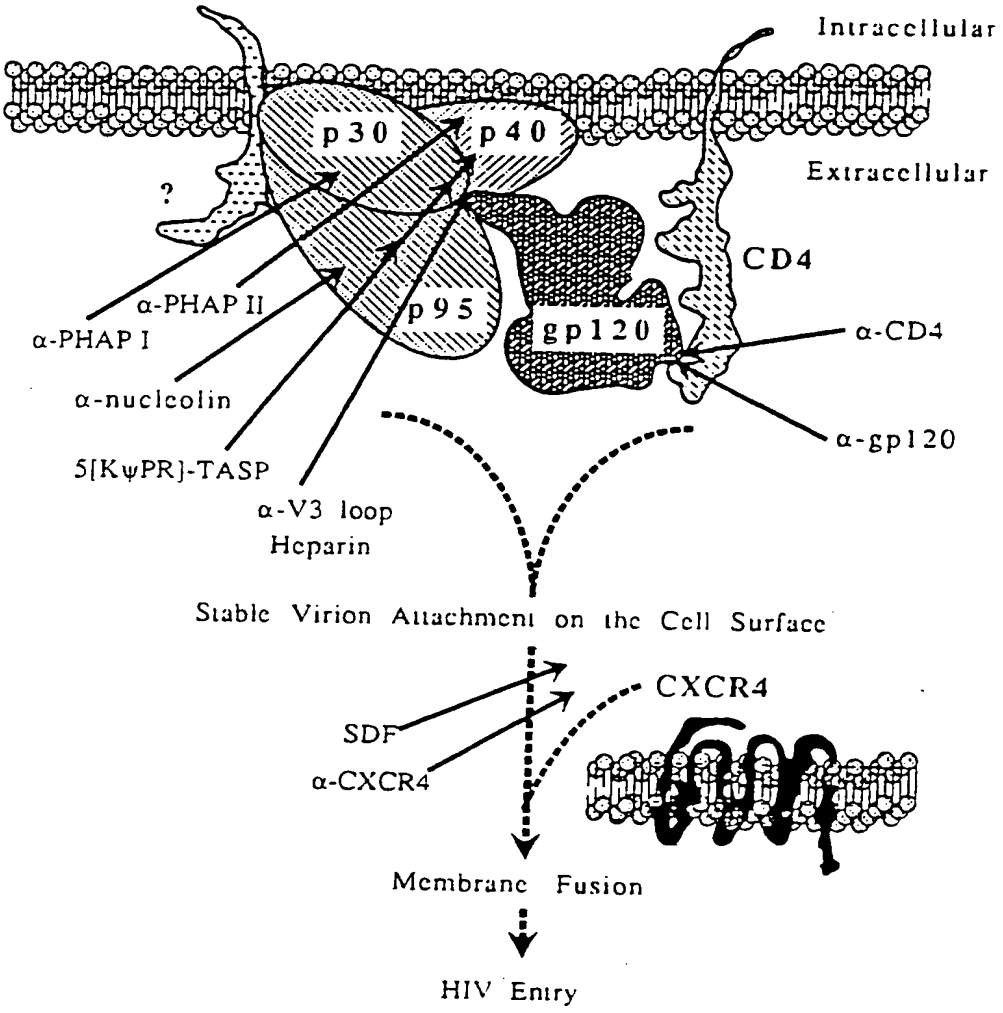

Intracellular
p30
p40
Extracellular
?
CD4
α-PHAP II
p95
gp120
α-CD4
α-PHAP I
α-nucleolin
α-gp120
5[KψPR]-TASP
α-V3 loop
Heparin
Stable Virion Attachment on the Cell Surface
CXCR4
SDF
α-CXCR4
Membrane Fusion
HIV Entry

FIGURE 22

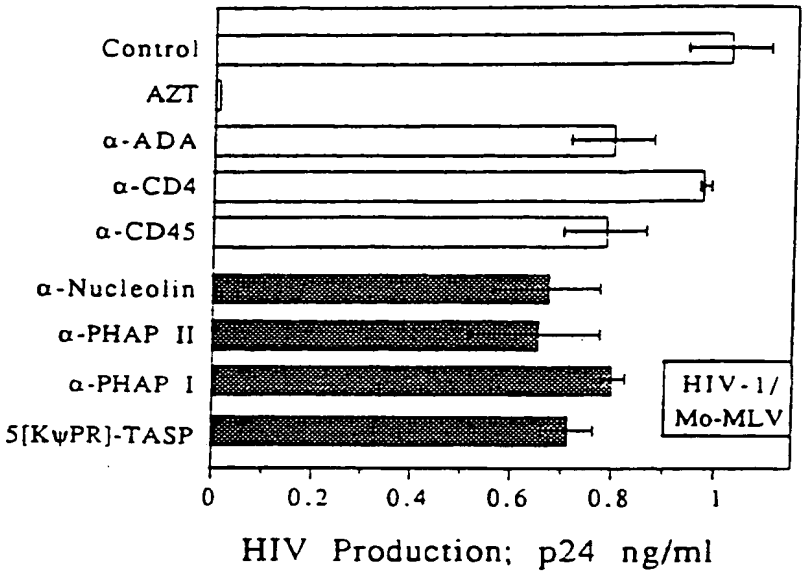

Control
AZT
α-ADA
α-CD4
α-CD45
α-Nucleolin
α-PHAP II
α-PHAP I
5[KψPR]-TASP
HIV-1/
Mo-MLV
0
0.2
0.4
0.6
0.8
1
HIV Production; p24 ng/ml

Figure 23

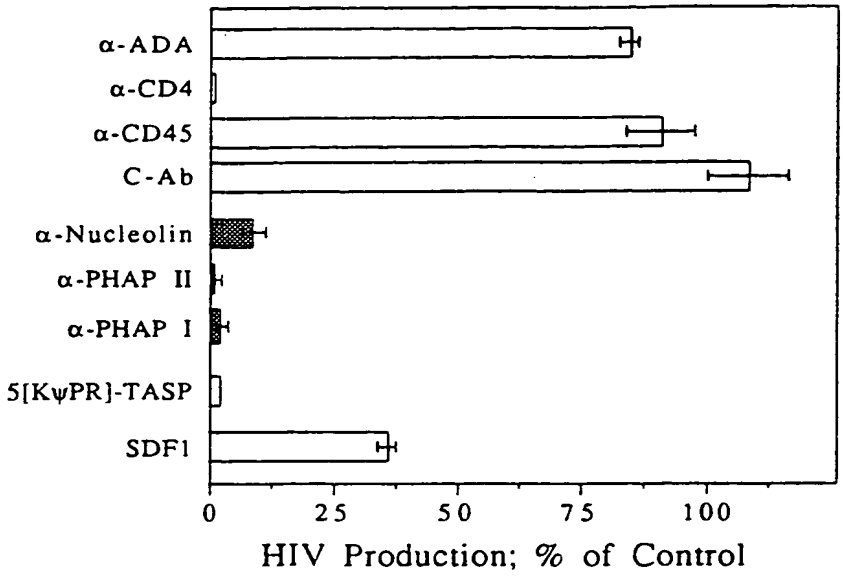

α-ADA
α-CD4
α-CD45
C-Ab
α-Nucleolin
α-PHAP II
α-PHAP I
5[KψPR]-TASP
SDF1
0
25
50
75
100
HIV Production; % of Control

Figure 24

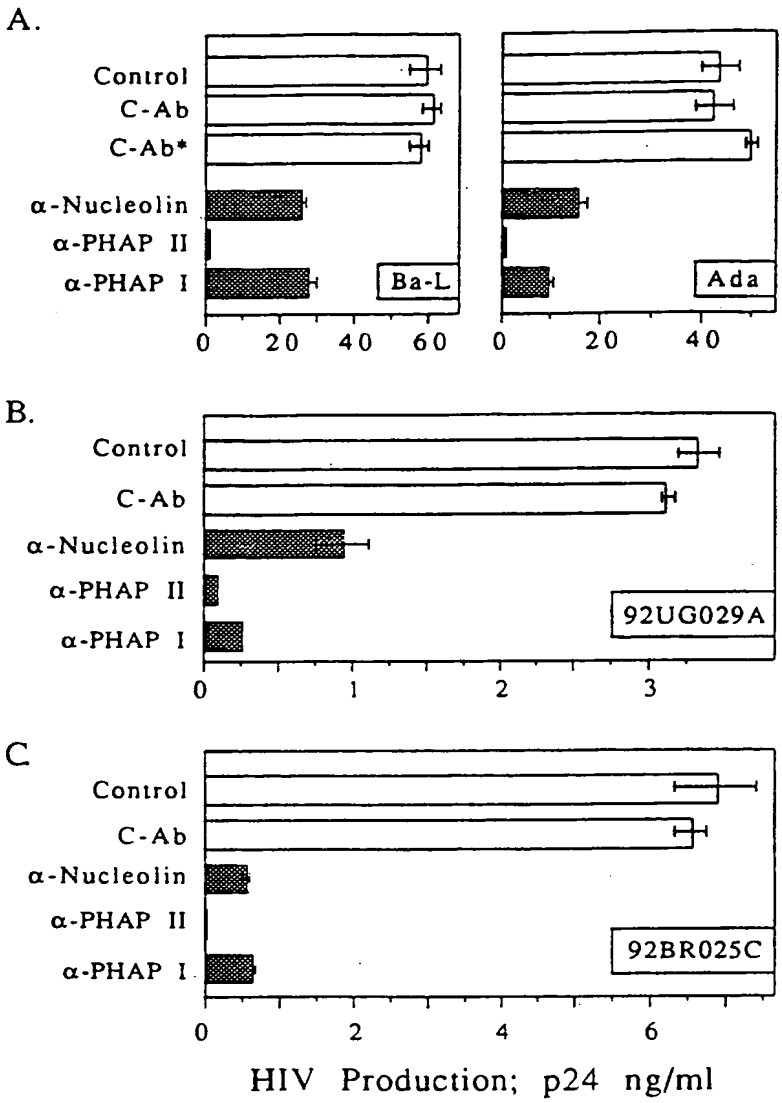

A.
Control
C-Ab
C-Ab*
α-Nucleolin
α-PHAP II
α-PHAP I
Ba-L
Ada
0
20
40
60
0
20
40
B.
Control
C-Ab
α-Nucleolin
α-PHAP II
α-PHAP I
92UG029A
0
1
2
3
C
Control
C-Ab
α-Nucleolin
α-PHAP II
α-PHAP I
92BR025C
0
2
4
6
HIV Production; p24 ng/ml

Figure 25

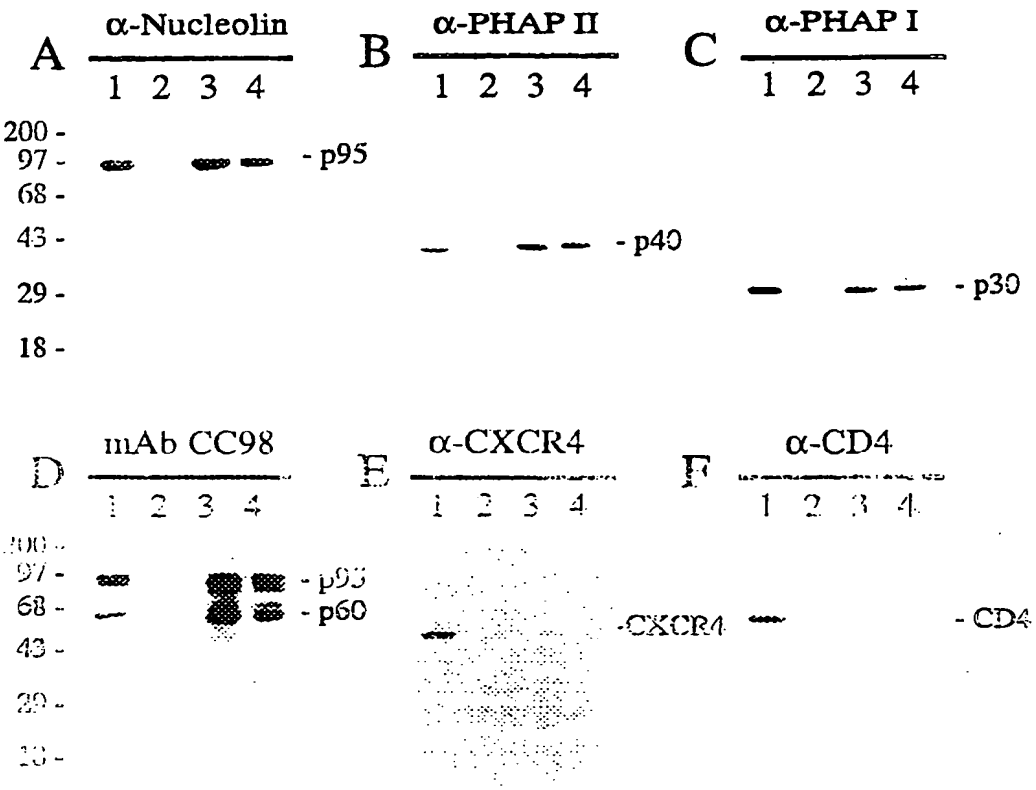

A
α-Nucleolin
1 2 3 4
B
α-PHAP II
1 2 3 4
C
α-PHAP I
1 2 3 4
200 -
97 -
68 -
43 -
29 -
18 -
- p95
- p40
- p30
D
mAb CC98
1 2 3 4
E
α-CXCR4
1 2 3 4
F
α-CD4
1 2 3 4
97 -
68 -
43 -
- p60
-CXCR4
- CD4

Figure 26

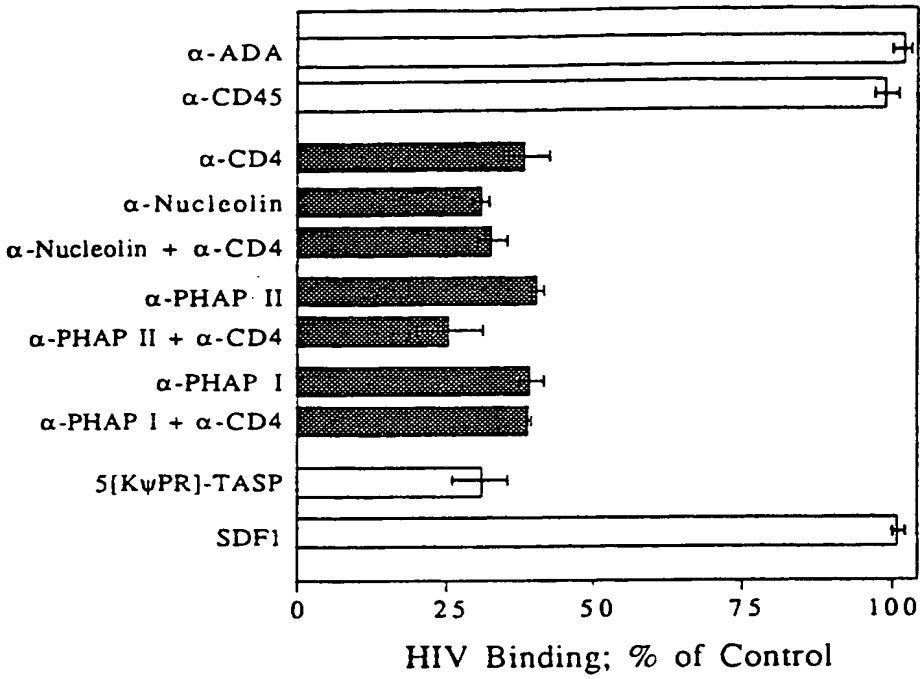

α-ADA
α-CD45
α-CD4
α-Nucleolin
α-Nucleolin + α-CD4
α-PHAP II
α-PHAP II + α-CD4
α-PHAP I
α-PHAP I + α-CD4
5[KψPR]-TASP
SDF1
0
25
50
75
100
HIV Binding; % of Control

Figure 27

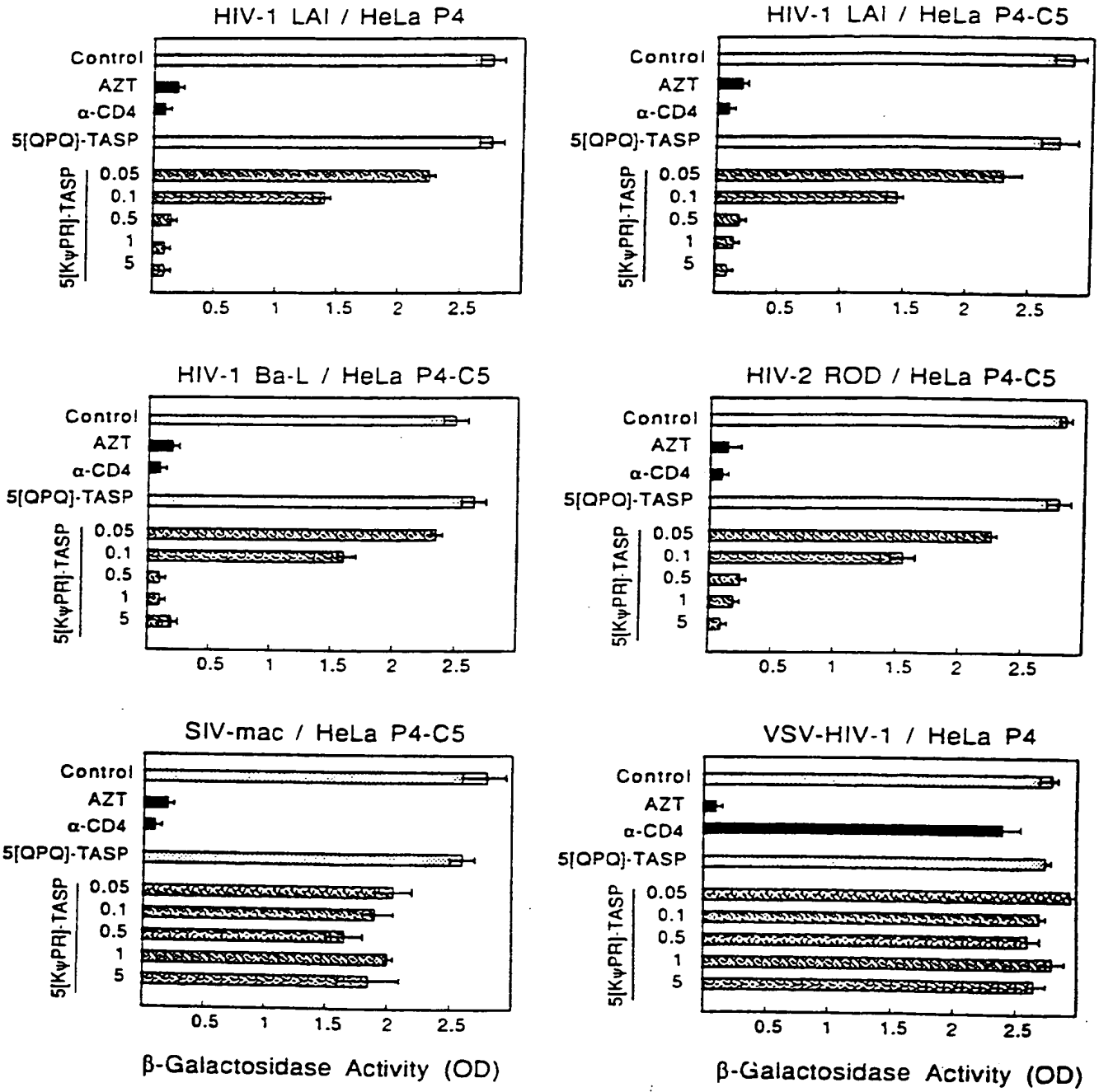

HIV-1 LAI / HeLa P4
HIV-1 LAI / HeLa P4-C5
HIV-1 Ba-L / HeLa P4-C5
HIV-2 ROD / HeLa P4-C5
SIV-mac / HeLa P4-C5
VSV-HIV-1 / HeLa P4
Control
AZT
α-CD4
5[QPQ]-TASP
5[KψPR]-TASP
0.05
0.1
0.5
1
5
0.5
1
1.5
2
2.5
β-Galactosidase Activity (OD)

FIGURE 28

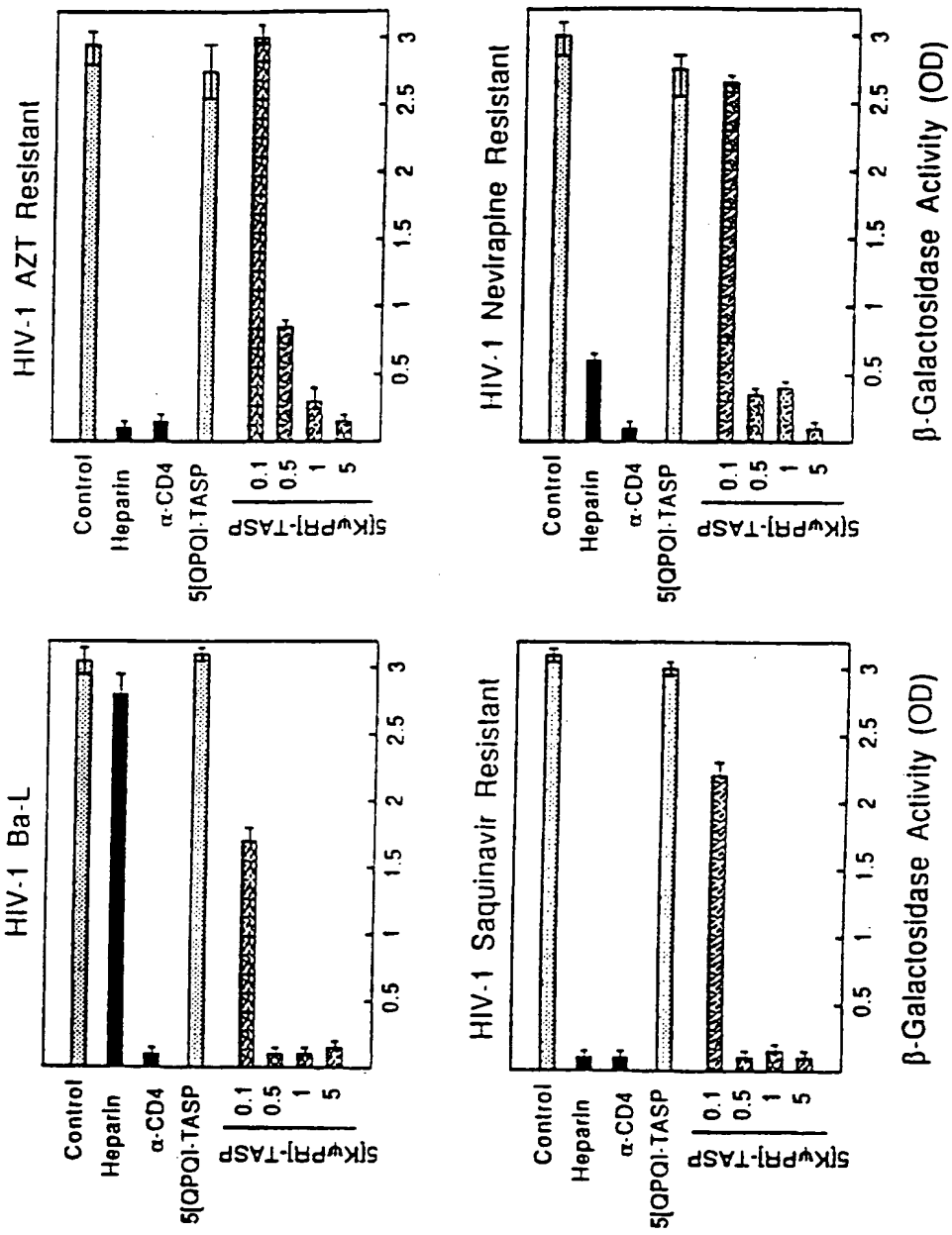

HIV-1 AZT Resistant
HIV-1 Nevirapine Resistant
HIV-1 Ba-L
HIV-1 Saquinavir Resistant
Control
Heparin
α-CD4
5[QPQI-TASP
5[KψPRI-TASP
0.1
0.5
1
5
0.5
1
1.5
2
2.5
3
β-Galactosidase Activity (OD)

FIGURE 29

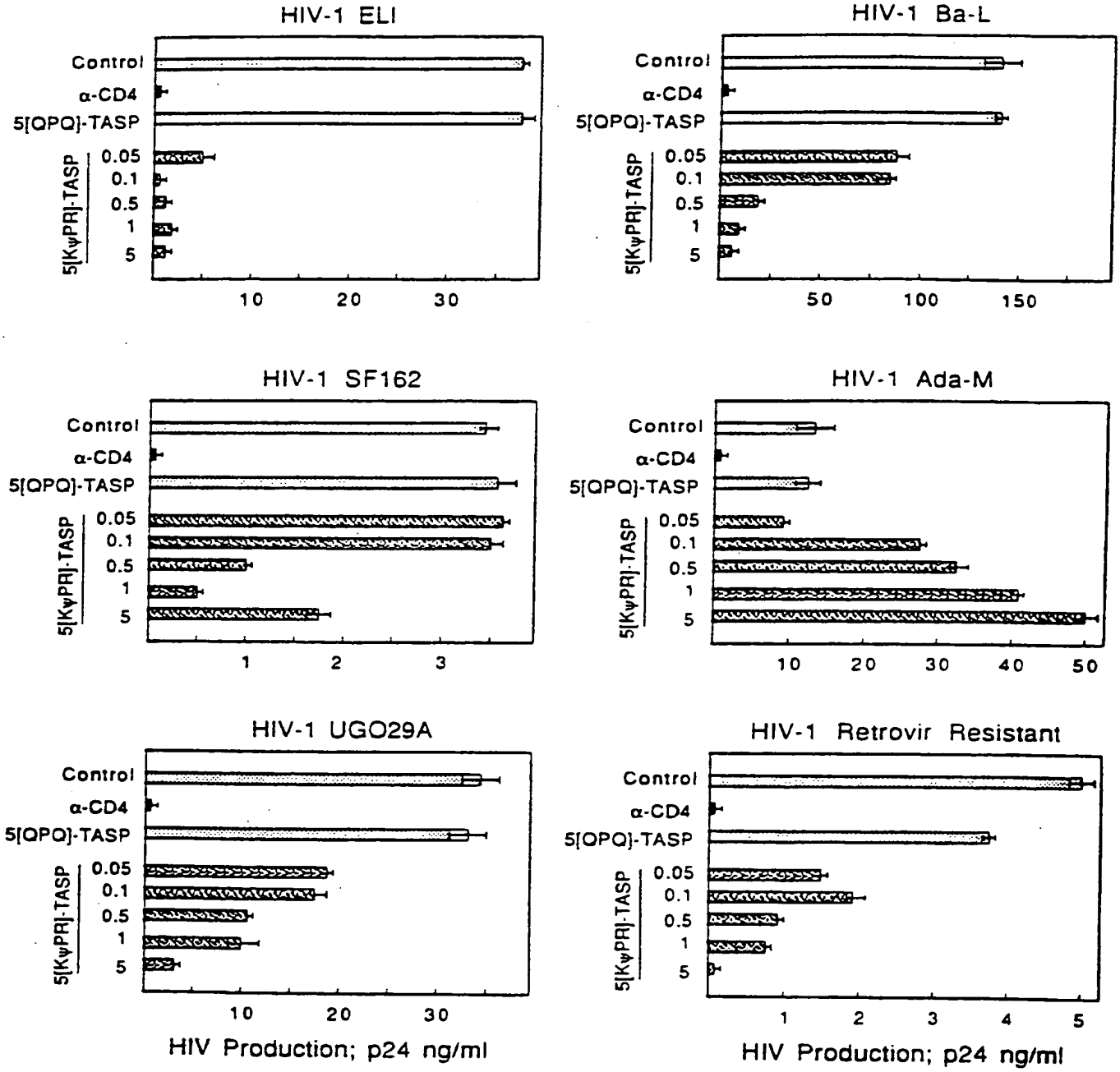

HIV-1 ELI
Control
α-CD4
5[QPQ]-TASP
5[KψPR]-TASP
0.05
0.1
0.5
1
5
10
20
30
HIV-1 Ba-L
50
100
150
HIV-1 SF162
1
2
3
HIV-1 Ada-M
10
20
30
40
50
HIV-1 UGO29A
HIV-1 Retrovir Resistant
HIV Production; p24 ng/ml
HIV Production; p24 ng/ml

FIGURE 30

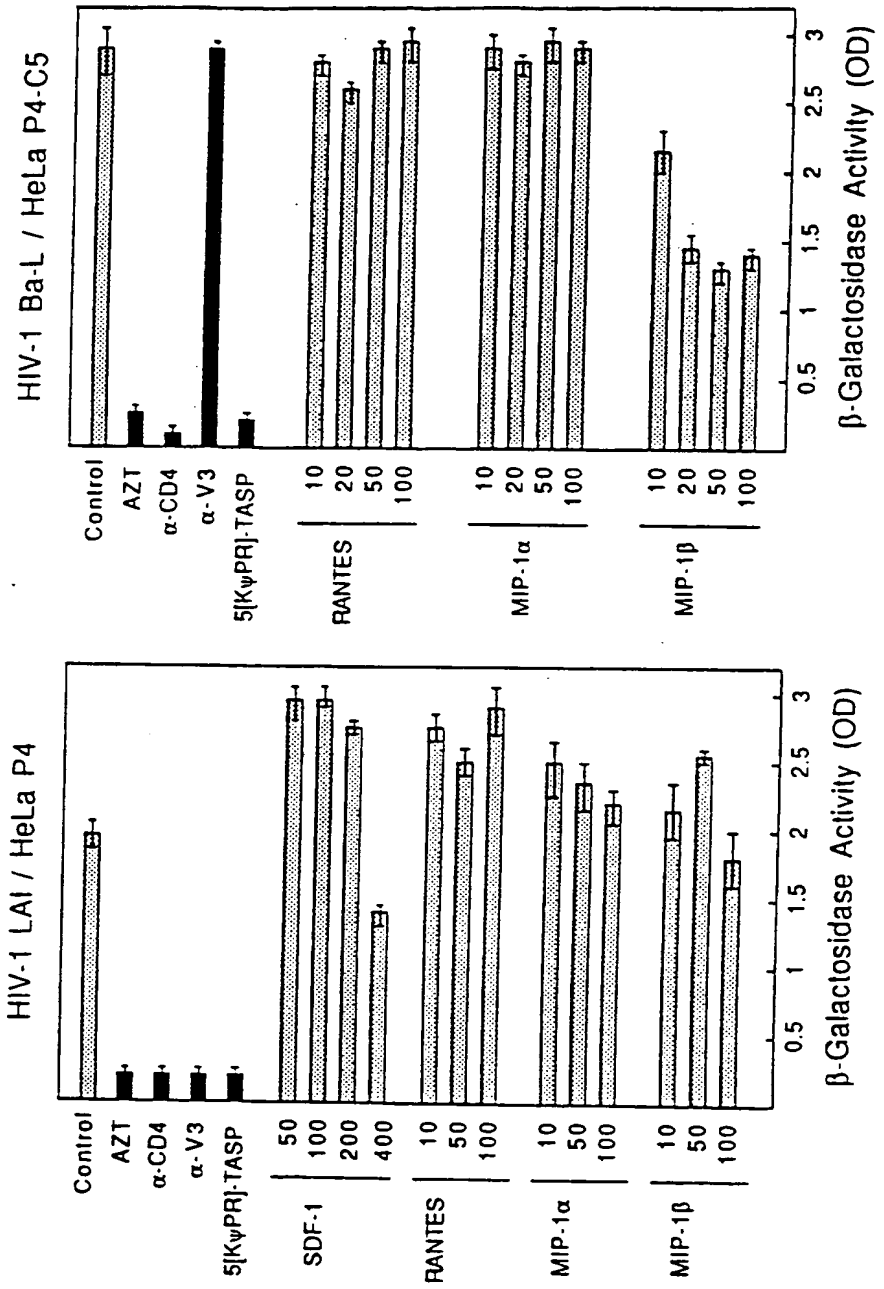

HIV-1 Ba-L / HeLa P4-C5
β-Galactosidase Activity (OD)
0.5 1 1.5 2 2.5 3
Control
AZT
α-CD4
α-V3
5[KψPR]-TASP
RANTES
MIP-1α
MIP-1β
10 20 50 100
HIV-1 LAI / HeLa P4
β-Galactosidase Activity (OD)
0.5 1 1.5 2 2.5 3
Control
AZT
α-CD4
α-V3
5[KψPR]-TASP
SDF-1
RANTES
MIP-1α
MIP-1β
50 100 200 400
10 50 100

FIGURE 31

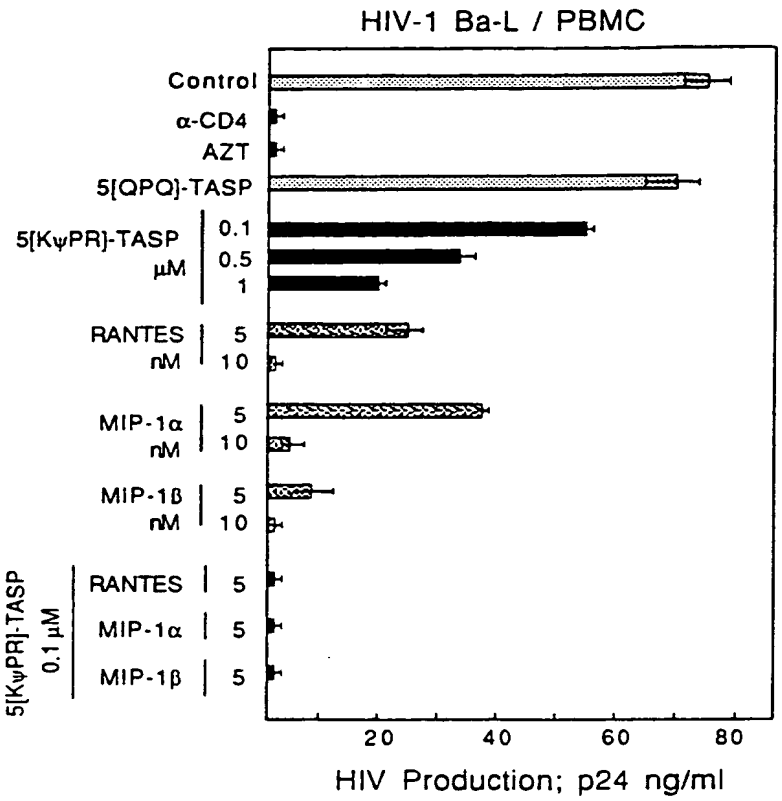

HIV-1 Ba-L / PBMC
Control
α-CD4
AZT
5[QPQ]-TASP
5[KψPR]-TASP μM
0.1
0.5
1
RANTES nM
5
10
MIP-1α nM
5
10
MIP-1β nM
5
10
5[KψPR]-TASP 0.1 μM
RANTES
5
MIP-1α
5
MIP-1β
5
20
40
60
80
HIV Production; p24 ng/ml

Figure 32

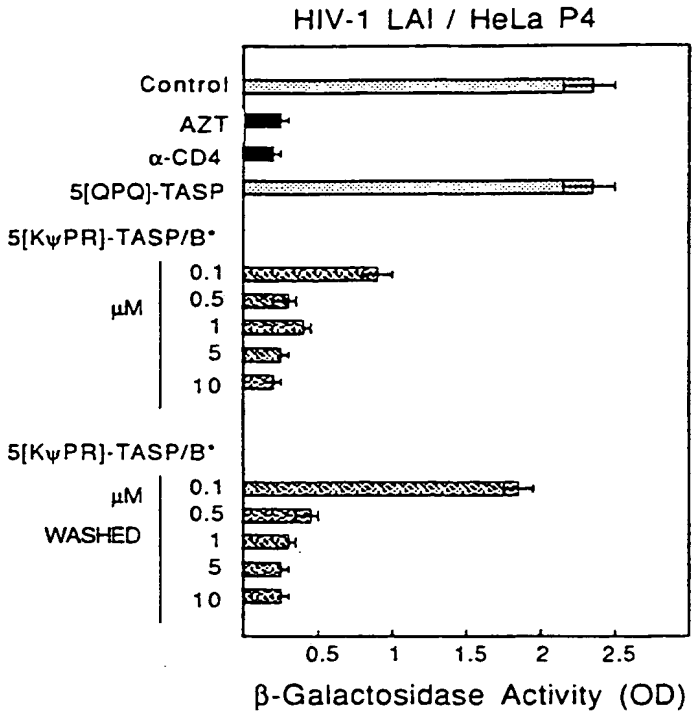

HIV-1 LAI / HeLa P4
Control
AZT
α-CD4
5[QPQ]-TASP
5[KψPR]-TASP/B*
μM
0.1
0.5
1
5
10
5[KψPR]-TASP/B*
μM
WASHED
0.1
0.5
1
5
10
0.5
1
1.5
2
2.5
β-Galactosidase Activity (OD)

Figure 33

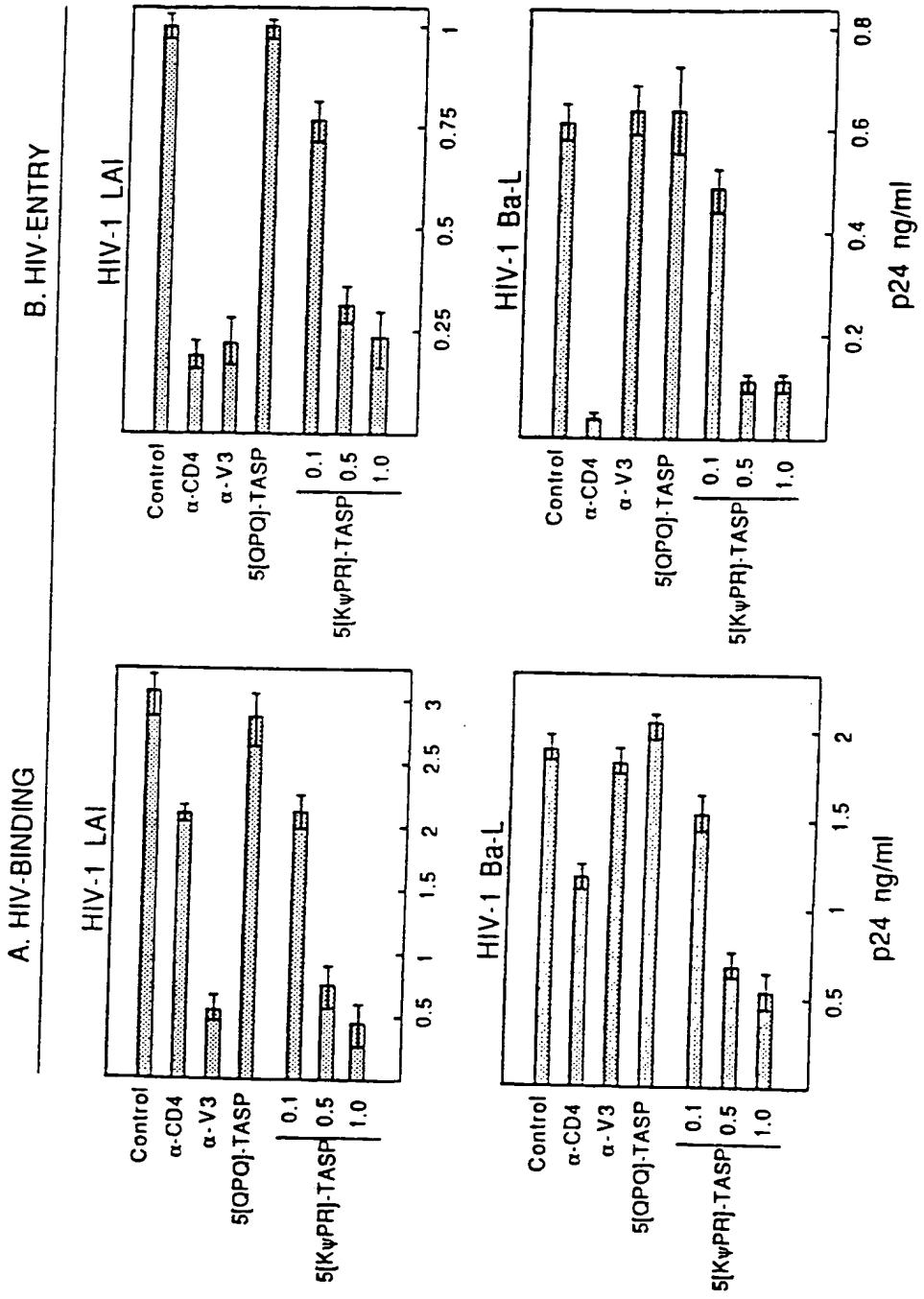

A. HIV-BINDING
B. HIV-ENTRY
HIV-1 LAI
HIV-1 Ba-L
Control
α-CD4
α-V3
5[QPQ]-TASP
5[KψPR]-TASP
0.1
0.5
1.0
p24 ng/ml

FIGURE 34

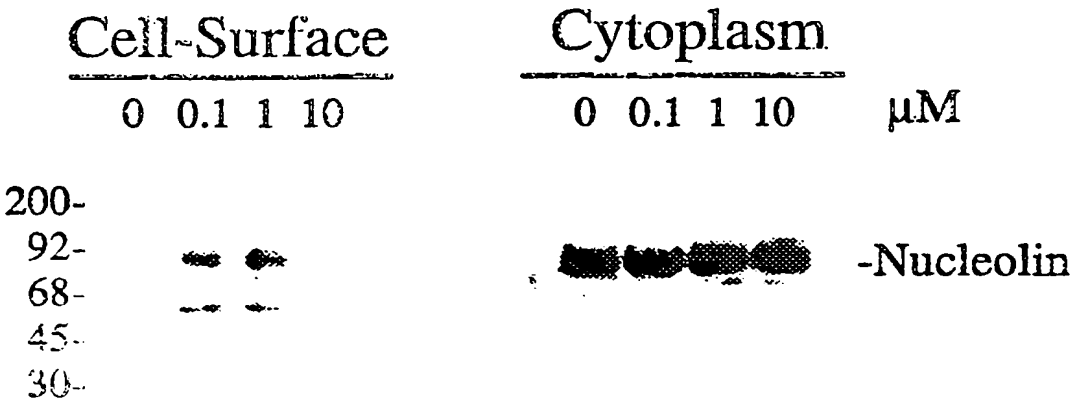
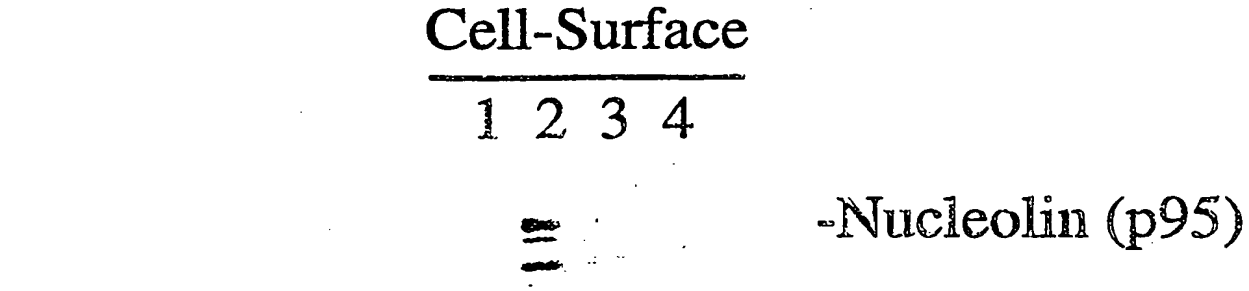

Cell-Surface
Cytoplasm
0 0.1 1 10
0 0.1 1 10
µM
200-
92-
68-
45-
30-
-Nucleolin

Figure 35



1: 1 hr; 2: 1 hr; 3: 6 hr; 4: 24 hr.
2, 3, 4: 5 μM

Figure 36

The effect of heparin at µg/ml on HIV infection in HeLa P4-C5 cells.

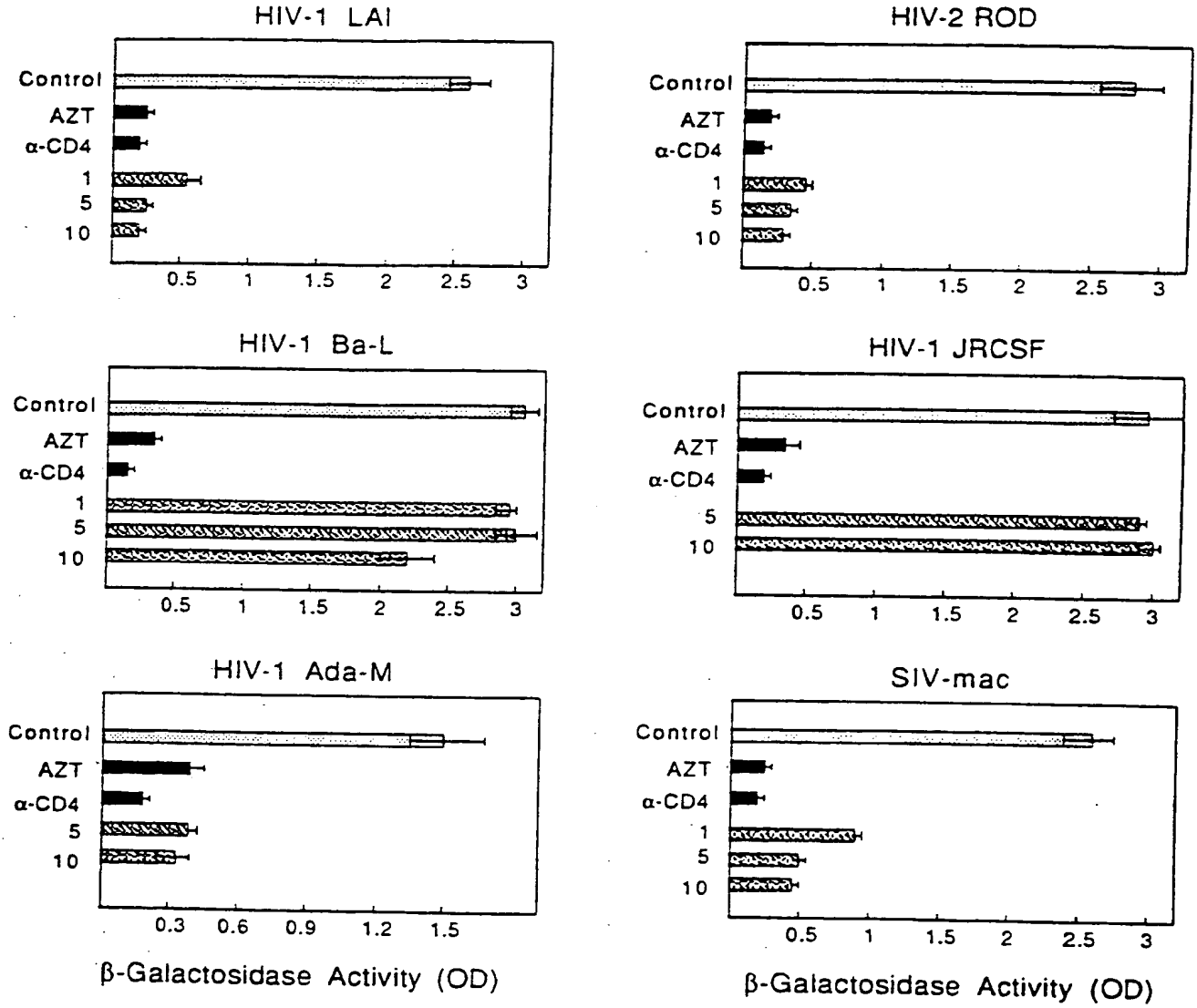


Figure 37

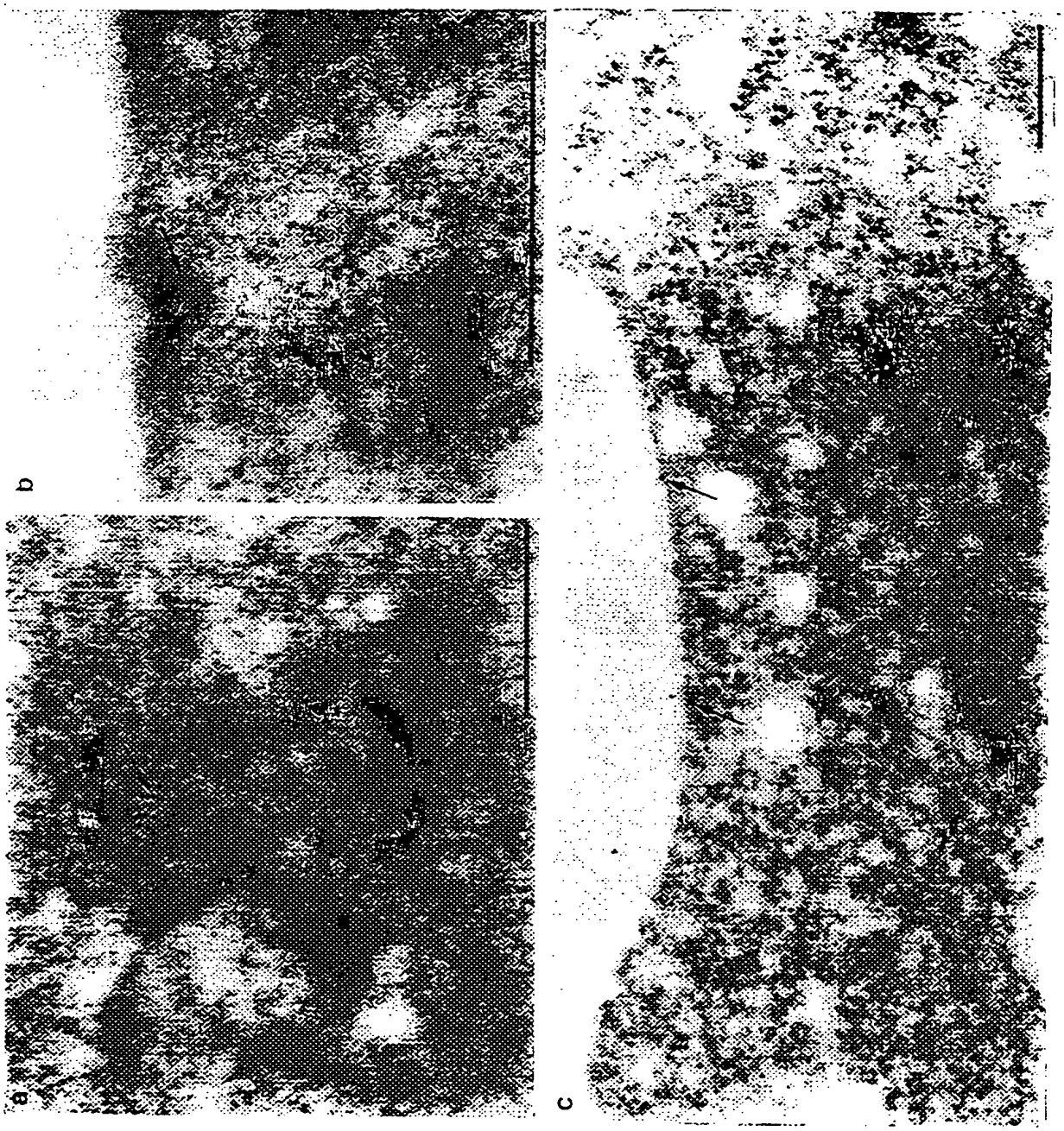


FIGURE 33

FIGURE 39

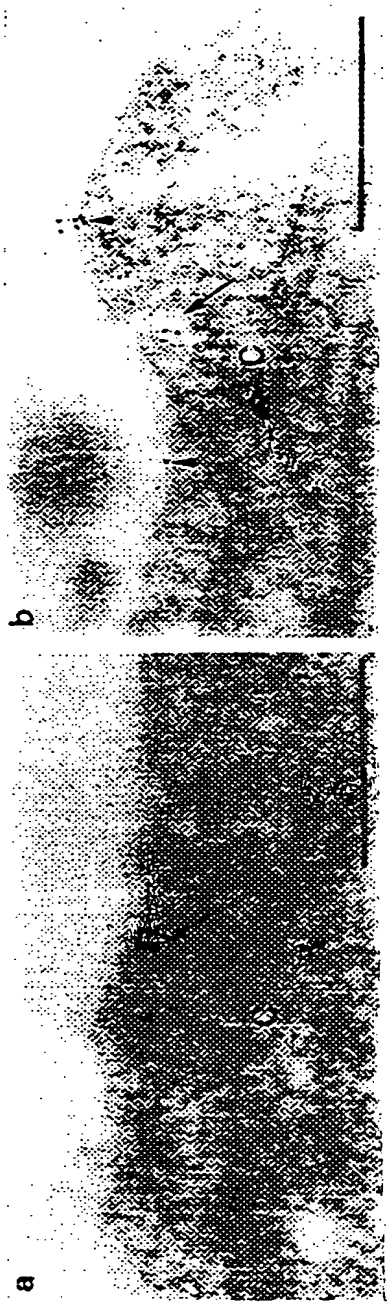


FIGURE 40A

FIGURE 40C

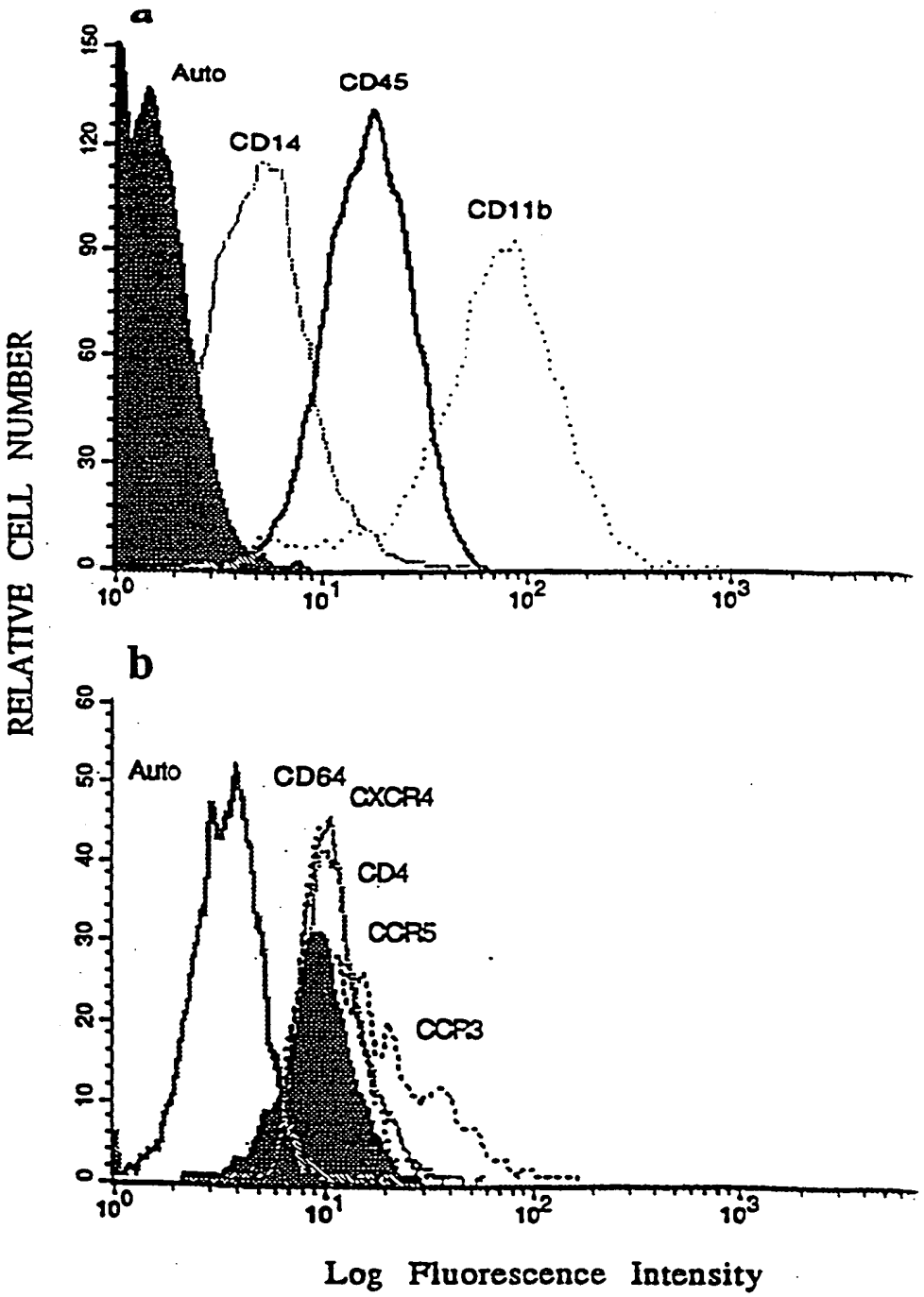

a
Auto
CD14
CD45
CD11b
RELATIVE CELL NUMBER
b
Auto
CD64
CXCR4
CD4
CCR5
CCP3
Log Fluorescence Intensity

FIGURE 41

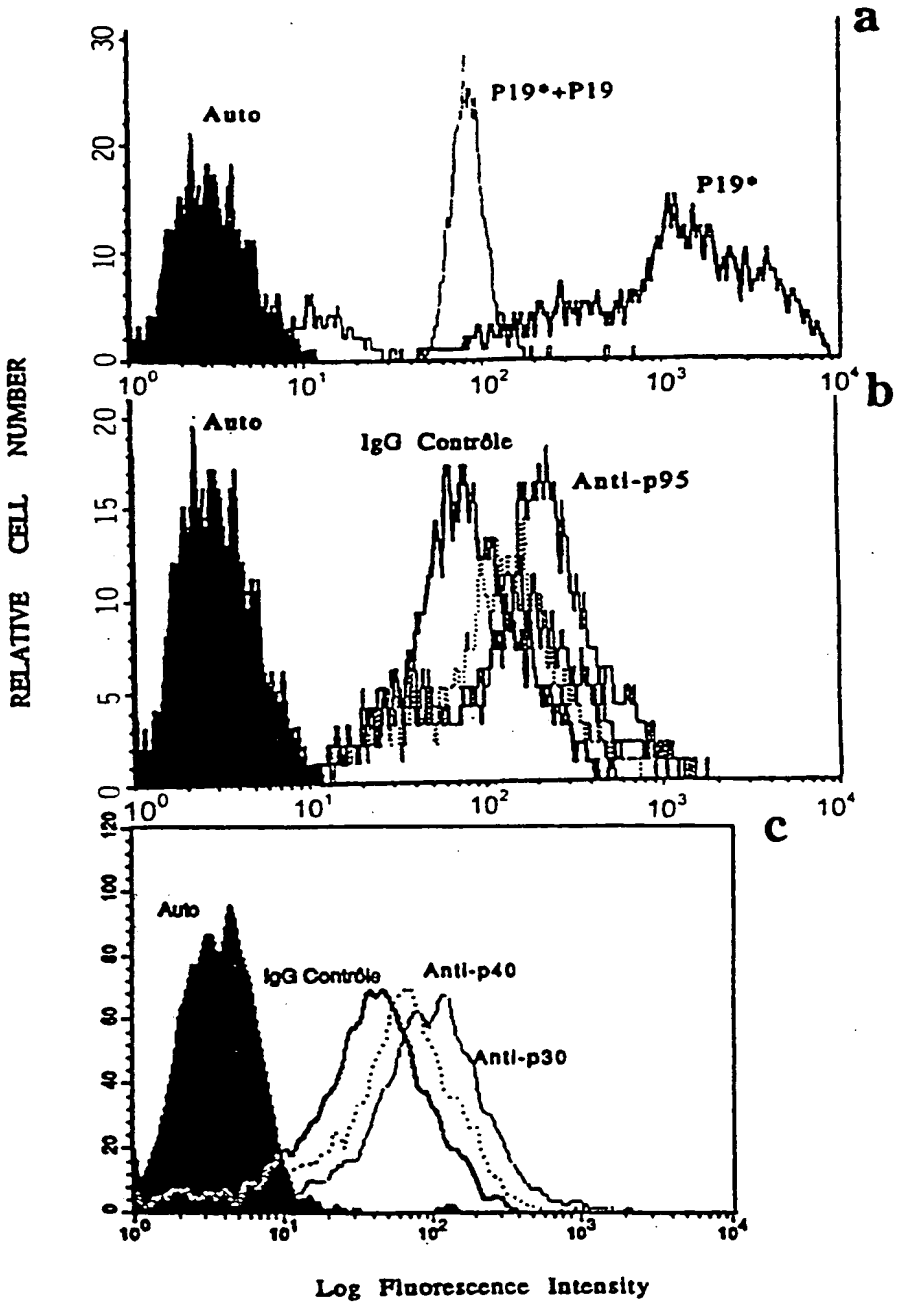

a
Auto
P19*+P19
P19*
b
Auto
IgG Contrôle
Anti-p95
c
Auto
IgG Contrôle
Anti-p40
Anti-p30
RELATIVE CELL NUMBER
Log Fluorescence Intensity

Figure 42

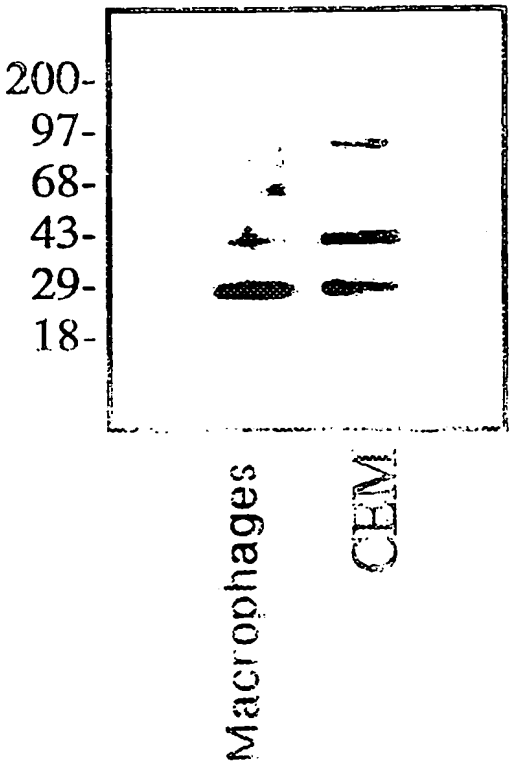


Figure 43

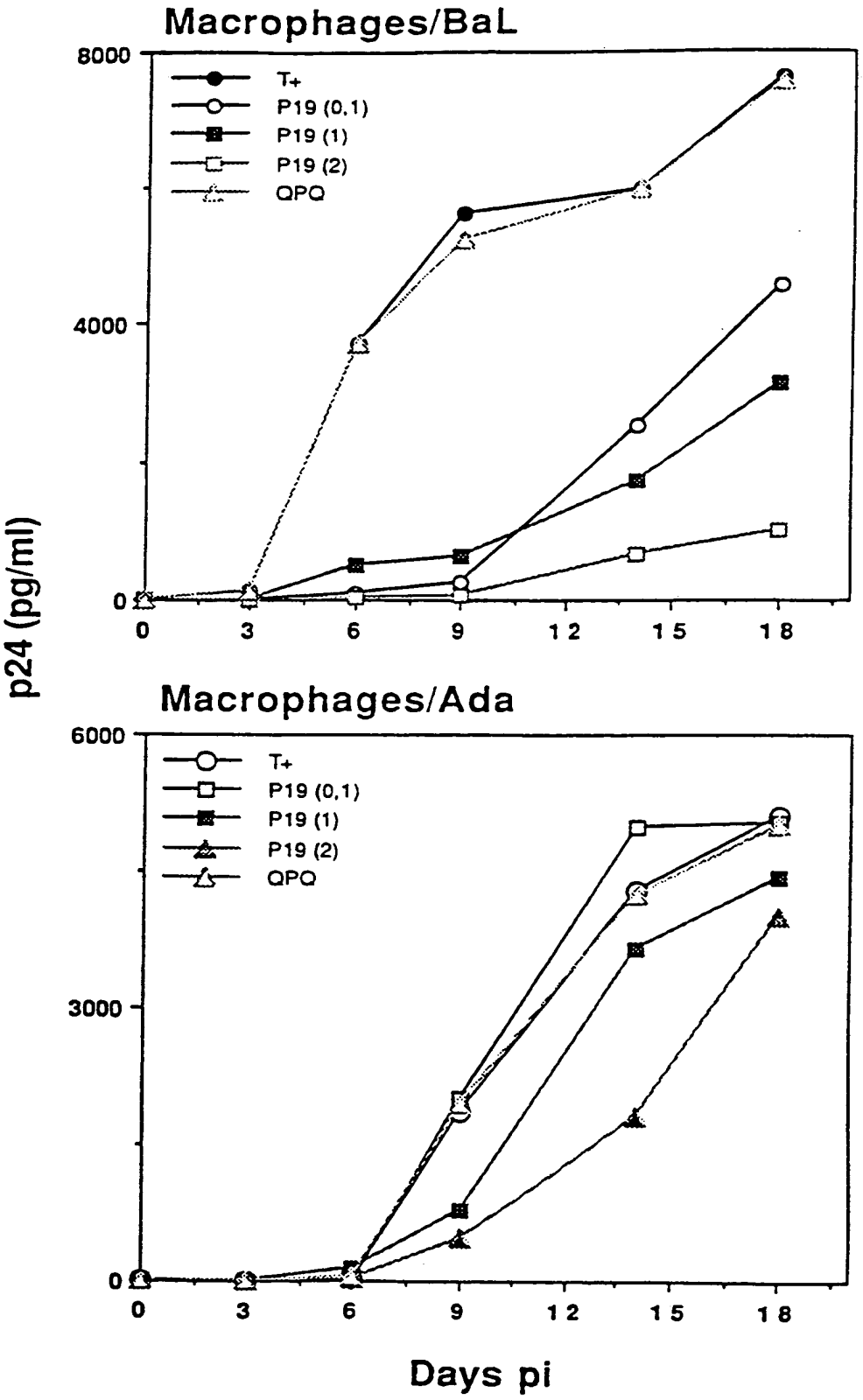

Macrophages/BaL
8000
4000
0
T+
P19 (0,1)
P19 (1)
P19 (2)
QPQ
0
3
6
9
12
15
18
p24 (pg/ml)
Macrophages/Ada
6000
3000
0
T+
P19 (0,1)
P19 (1)
P19 (2)
QPQ
0
3
6
9
12
15
18
Days pi

FIGURE 44

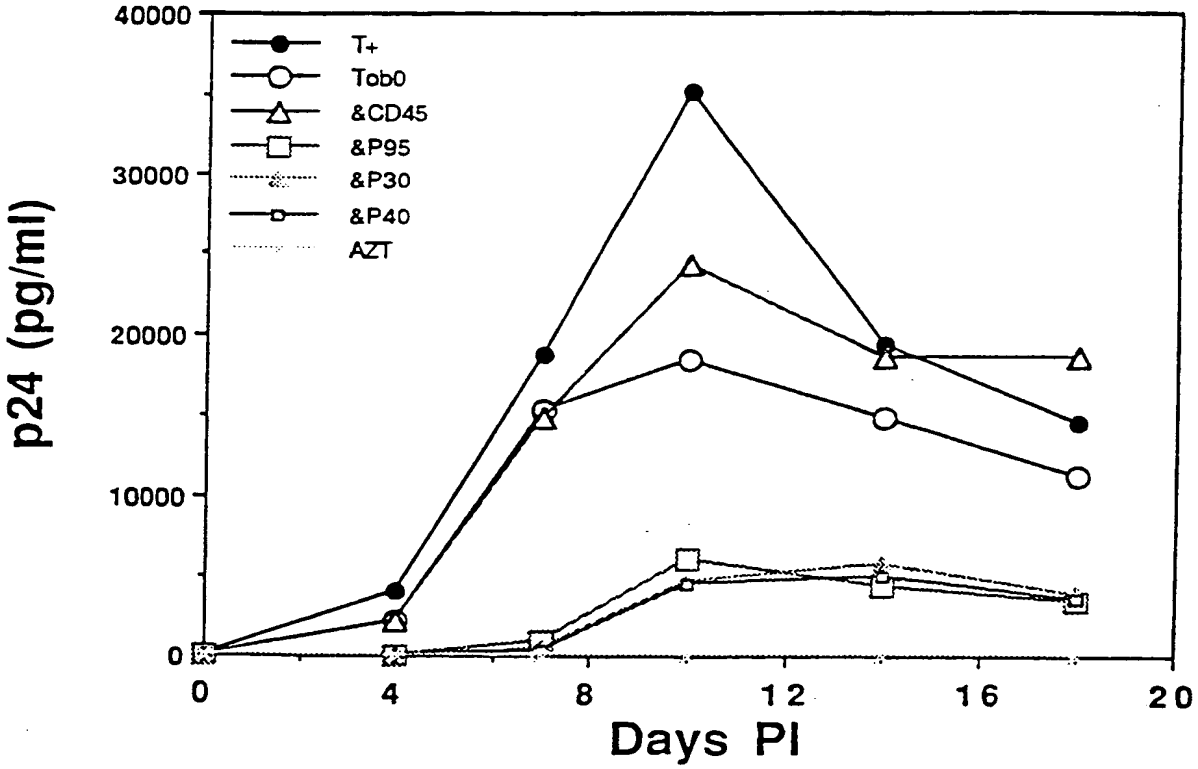

40000
30000
20000
10000
0
p24 (pg/ml)
T+
Tob0
&CD45
&P95
&P30
&P40
AZT
0
4
8
12
16
20
Days PI

FIGURE 45

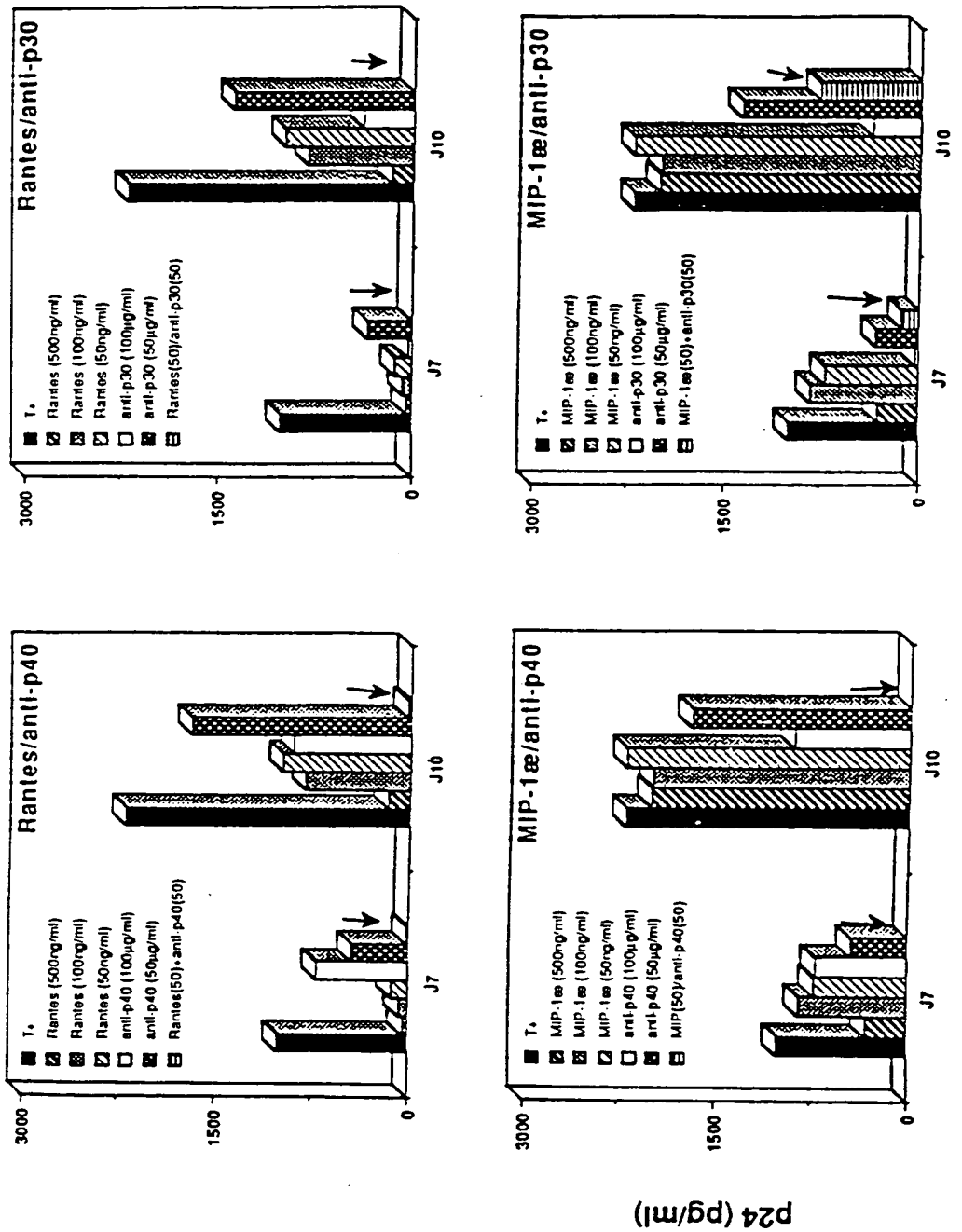

Rantes/anti-p30
MIP-1æ/anti-p30
Rantes/anti-p40
MIP-1æ/anti-p40
T.
Rantes (500ng/ml)
Rantes (100ng/ml)
Rantes (50ng/ml)
anti-p30 (100µg/ml)
anti-p30 (50µg/ml)
Rantes(50)/anti-p30(50)
MIP-1æ (500ng/ml)
MIP-1æ (100ng/ml)
MIP-1æ (50ng/ml)
anti-p30 (100µg/ml)
anti-p30 (50µg/ml)
MIP-1æ(50)+anti-p30(50)
anti-p40 (100µg/ml)
anti-p40 (50µg/ml)
Rantes(50)+anti-p40(50)
MIP(50)/anti-p40(50)
3000
1500
0
J7
J10
p24 (pg/ml)

FIGURE 46A

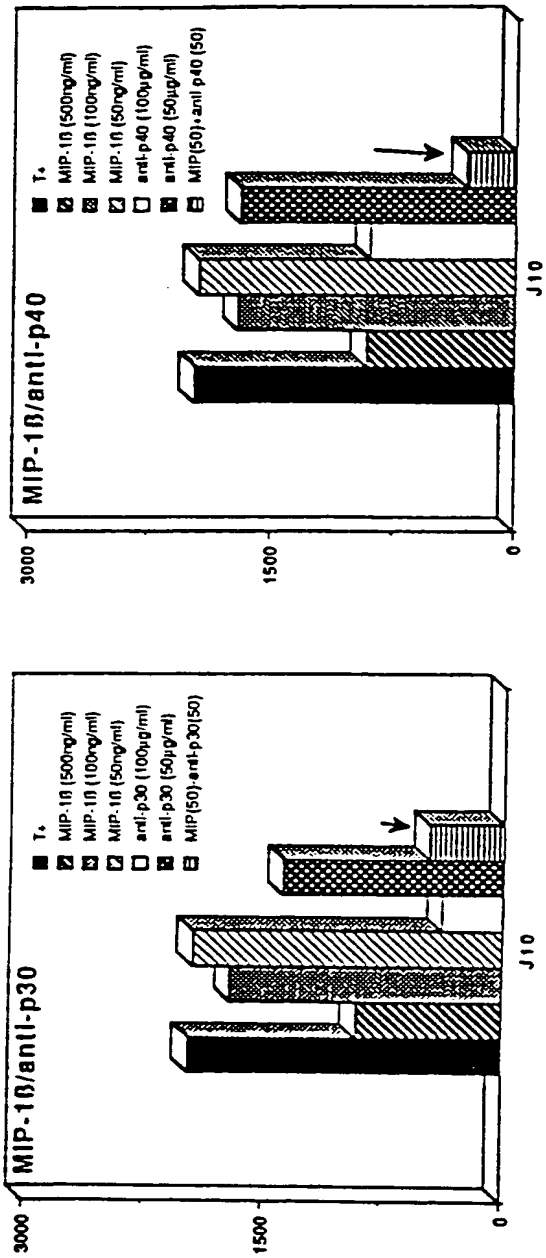

MIP-1β/anti-p40
T.
MIP-1β (500ng/ml)
MIP-1β (100ng/ml)
MIP-1β (50ng/ml)
anti-p40 (100µg/ml)
anti-p40 (50µg/ml)
MIP(50)+anti-p40 (50)
3000
1500
0
J10
MIP-1β/anti-p30
T.
MIP-1β (500ng/ml)
MIP-1β (100ng/ml)
MIP-1β (50ng/ml)
anti-p30 (100µg/ml)
anti-p30 (50µg/ml)
MIP(50)+anti-p30(50)
3000
1500
0
J10

FIGURE 46B

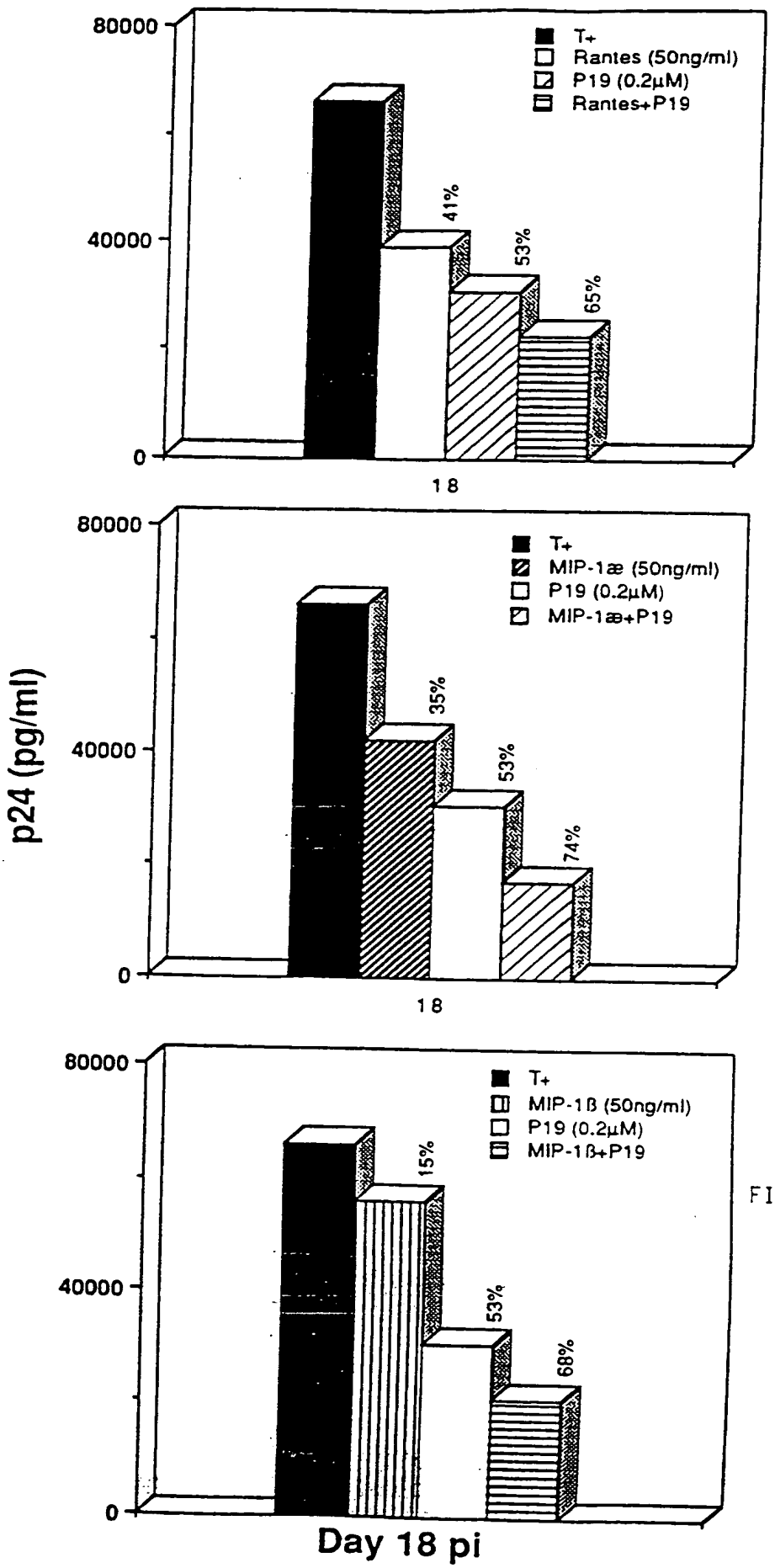

80000
40000
0
T+
Rantes (50ng/ml)
P19 (0.2µM)
Rantes+P19
41%
53%
65%
18
80000
40000
0
T+
MIP-1æ (50ng/ml)
P19 (0.2µM)
MIP-1æ+P19
35%
53%
74%
18
p24 (pg/ml)
80000
40000
0
T+
MIP-1ß (50ng/ml)
P19 (0.2µM)
MIP-1ß+P19
15%
53%
68%
Day 18 pi

FIGURE 47

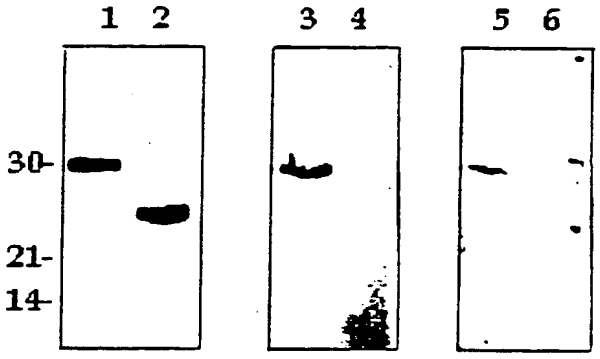


Figure 48

FIGURE 49(1)

I.

/translation="MVKLAKAGKNQGDPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGE
EVVIPQKKGKKAAATSAKKVVVSPTKKVAVATPAKKAAVTPGKKAAATPAKKTVTPAK
AVTTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEEDDDSEEDEEDD
EDEDEDEDEIEPAAMKAAAAAPASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAKG
KKAAKVVPVKAKNVAEDEDEEEDDEDEDDDDDEDDEDDDDEDDEEEEEEEEEPVKEA
PGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKN
DLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGKDSKKERDA
RTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADAEKTFEEKQ
GTEIDGRSISLYYTGEKGQNQDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEK
ATFIKVPQNQNGKSKGYAFIEFASFEDAKEALNSCNKREIEGRAIRLELQGPRGSPNA
RSQPSKTLFVKGLSEDTTEETLKESFDGSVRARIVTDRETGSSKGFGFVDFNSEEDAK
EAMEDGEIDGNKVTLDWAKPKGEGGFGGRGGGRGGFGGRGGGRGGRGGFGGRGRGGFG
GRGGFRGGRGGGGDHKPQGKKTKFE"

II.

```
   1  ATTCTGCTGT AGACATAGAG ATGATGATCA TAGCTGACTA TGATGATGAT
  51  CCCCCGCGAG CCTGAAAGAG GAAATGCTCT GGTTTGCTAA GCCCGCGAAT
 101  CGAGTGAGAC CCACCCACAA AGCTAACCGT GGAAGTCACT GGCGGCCTCC
 151  TTCGCCCTGC CAGCCGGGGA ACCCATCCGG TGGCTCTCGA CCTGCTCCCG
 201  GGCCATCTGG TGACACTGAC TTCGCAGCCA CCACCTTAAT TGGCGCATTC
 251  GACCCAAATA ATAACCTGGG AACCTGTGGG CGGTCTAAGG CCCGGCTCTG
 301  CGGTCGCCCT CCCAGGCCCC TCTCCCTGGC CCTGTGAGGC CAGAAAGTTA
 351  CTTCTCCGAG GCCAGTTCCC CATGTCTGAG AAATATCTCC CAACTTGAGG
 401  TTCTGTGGGG TAGGGGAGGG TTCGTGACTT TCTCACAGAA AACCTCGTAC
 451  AGACCCCGCC ACTGCCTTTA TTAACAGCTC TCAGGAGACT GCCTGCAGGA
 501  GGGGGGTCGC TCCGGCCCCA TGCTCGCGGG CAAGCAGGGA TAAGCTGTGC
 551  CTCCAAAAGG GCCAACGGGA ACTCCGCGGT CCCTGAACTT CCGGTGCTGG
 601  AGGACTCCTC GCTCCAGGGC CACCAGGAGC CGCGGCGTGA GTGCGTGCCG
 651  GAACCGAGGG CGGGGTCTCT GAGGAACTCC AAGGCTGCCC AAGCCTACGG
 701  ACCCAGCCAC ATTGGCGAAC CGGAGACCGC CCGATTCCAC CACCCCCGCG
 751  CTCCCCTCAC AGCCGGCGCC AAAAACGCCA GTCCCACGAC GCAGGCCGGG
 801  ACCCGCGCGC CCACGGCCCA ATCAGCGCGA CCTTGCACAA AGCGAGCCCC
```

FIGURE 49(2)

```
 851  GCCCCCACGG CGCCGTTGCC AGCCCCTCCC CCTCCCGTGC CGCCTCGGCC
 901  CGCCTACTCC CCGCCCCGCG CCGTTCACGG TTAGAGGCTC GCGATTGGCT
 951  CATGGGGACG GCCGCGAGCT TTGGTTGGTC GGCGCGGAGT CACGAGGCGC
1001  CGTCGTCGCC TTTCCACAGG CGTTACTGGG CAGGCTCAGT CTTTCGCCTC
1051  AGTCTCGAGC TCTCGCTGGC TTCGGGTGTA CGTGCTCCGG GATCTTCAGC
1101  ACCCGCGGCC GCCATCGCCG TCGCTTGGCT TCTTCTGGAC TCATCTGCGC
1151  CACTTGTCCG CTTCACACTC CGCCGCCATC ATGGTGAAGC TCGCGAAGGT
1201  AAACGGCCTT GAGCGCGACG CAGACGTGTA GGCCTGCTTC CGAGGGCGA
1251  GCGCGGCGCC GCGGGGAGGA GGGCCTGCGC GCAGTCCCGG GCGCGTTCTA
1301  GGGCGCCATG CTGCGGGAAG TCTCGCGCGA TTAGTGGGGA GGTCTCGCGC
1351  TTCTGGCTAC TTGGTGGCGA GGTGAAGAGC TTCTGCAGGT GCTGGGGGAG
1401  GGGGCGCTGG GCCTCGGGGT GGAGAGATGA GACCAAACTT TTGCGACGCG
1451  TACGAGCTGG GACTGACTCT GACGCACGTG CCCGGGAGCG TGCCTGCCAC
1501  GTGGGCCGGC GTAGGTCTGG AATCTCCAGA GGGACCGGGT GCCTTGGGCC
1551  GGGAAATGGC GGTATCGGCC CTAGTCGGAG TCCCGGCTGC GCTCGGATGT
1601  CTCCGCCCCG GCCTGGCAAG CCGATACGTG GTGGGCCCCG GAAGGTGGCT
1651  CTGCCGCGTG CCTTTTGCGC TGTGTTTCGG GCAAGAGGTG GTCCTGCCAG
1701  GTACCCCCAC GTGGCCGCAC CCGCCTCTTT AAGGGGCGGG GTAGTGCTGG
1751  GGAAAGGCAT AAGCTTCATG AGAAAATAAG GTAGTATTTT TAAGTGCCTT
1801  AATGATCTTC ACCGTTAATT TGATTCAAAT AAGGGTGGTA GATAAAGTAC
1851  CGGGATTTGT AGTATAAAAA CACGGTTGTG CTTAACTAAG GTAACGGGAG
1901  GAGAAATCAT TTCCTCAGGT TGACTTTTTA CCTTAGGGCA GGTTTTCTGT
1951  TGGTAAAGCC TGGGAGGAAA AATGTGGGCG GTTGAGAAGT AGTCCCTCTT
2001  GCATTGCCAT CAGGAGTAGT TTCTATGTTA GTTGTGGTGT TTGGCACTAT
2051  GAGAAATGAT CTGAGACGGA GATGATGGCG TATGAACACT AATGGCAAAA
```

FIGURE 49(3)

2101 TATGAATGGC CTGAAATGTC GAGGTGGAGG TGTAATGATC TATTTGTGTC

2151 CATTTTAGGC AGGTAAAAAT CAAGGTGACC CCAAGAAAAT GGCTCCTCCT

2201 CCAAAGGAGG TAGAAGAAGA TAGTGAAGAT GAGGAAATGT CAGAAGATGA

2251 AGAAGATGAT AGCAGTGGAG AAGAGGTAAT TTTATCCAAC TTAATGCAGA

2301 ATTATGTTAA AACTACAAAA TGGAGAGTTA AGACATGAAA TTGGATATCT

2351 GTGGCAAAAA TAAGATTTTA TCAGGTATGT CTTATTGTAG TGGTTGAGTG

2401 TTTCACAAGC TCTTCATTGA CATGTCAAGA TGTCATTTGG CTAGTATTTG

2451 AATGTGAGTG CTAAGACGAG ACTGGGAATT TCTTTTACAT GTTCCTCTGC

2501 AGGGCTTGGA GTGTGATTTG TTGTGTTAAA TCATTACATT TTTCCAGTTT

2551 CAACATGTTA GCTCACCCCC ACATGTAGAG CTGGGCATTG TATTCAGAGC

2601 TGAGAATAAC CTTACCAGAT TCCTTTCCTA TCCTCCGAAT TAAAATTAAT

2651 TGGTCTCCAT TCCATATATA TATAACTGTA TCACTACTGG TTAAGTACTC

2701 GGGTGTAGAC TGAGGGCTGC CACCTCTCTT TGGTACCATT GACCCTCTTT

2751 AGCCACCTCC TGGCCTTTTA TTTGCCTCCA CTATAAAGAC AGCTGAGCAC

2801 TGAATTGTGC TCAGGTTTTC GTTGAGAACC TGAATGAAAG TTTTACTCTC

2851 CACACATTGC CTTGATAAAA CTACGGGATT TTAATGTAGC TAAATGATGA

2901 CTTTTATCAA ACTACCATGC ACACTCTTTG ATGTGTGATA GTTTTGTAAG

2951 GAATATTTAT ATTTAGCCTA TTCATTTTTT GTCTCAGGTC CTAAGAATTG

3001 AGCTTCACTG GGCTTGGTGG ACCGCAACCA CGAGGGCCCC AATGATTTAA

3051 TAAGTTAATG CTTGGAGCCT CCTATGTGTA ACGTTCTGAA TAATTTACAC

3101 ATAGCAATTC ATGACCTTAA ACATGTAAGG ATGATACTAT TACCATTTTC

3151 AGATGAGAAA GTTGGGGCTT GGGAAAGTAT GAGGTGTAAG AATTCAGAGG

3201 GTCTGGTTCA GAGGTATTTT CAGTGTTCAA AAGAGTTCCT TATGTCTGGG

3251 TATTCACCTT ATTATAGGGG CTCTGACTTA AGACAACATA ACAGAAGCCT

FIGURE 49(4)

```
3301  GGAGTTTTAA CATGTCATAT GTGTCATGCG TATGTCTTGA ACCAGAGGCA
3351  TTGCCAGAGT CTAACAACTC ATTGGGACCA TGGTTATCTT TTTGGGTGTG
3401  GGGCTGGACT TACTGGTTTG GTTTTCATTT ATCTCAAGGT CGTCATACCT
3451  CAGAAGAAAG GCAAGAAGGC TGCTGCAACC TCAGCAAAGA AGGTGGTCGT
3501  TTCCCCAACA AAAAAGGTTG CAGTTGCCAC ACCAGCCAAG AAAGCAGCTG
3551  TCACTCCAGG CAAAAAGGCA GCAGCAACAC CTGCCAAGAA GACAGTTACA
3601  CCAGCCAAAG CAGTTACCAC ACCTGGCAAG AAGGGAGCCA CACCAGGCAA
3651  AGCATTGGTA GCAACTCCTG GTAAGAAGGG TGCTGCCATC CCAGCCAAGG
3701  GGGCAAAGAA TGGCAAGAAT GCCAAGAAGG AAGACAGTGA TGAAGAGGAG
3751  GATGATGACA GTGAGGAGGA TGAGGAGGAT GACGAGGACG AGGATGAGGA
3801  TGAAGATGAA ATTGAACCAG CAGCGATGAA AGCAGCAGCT GCTGCCCCTG
3851  CCTCAGAGGA TGAGGACGAT GAGGATGACG AAGATGATGA GGATGACGAT
3901  GACGATGAGG AAGATGGTAA GGAGTTGTCT TGGTAGTTAC TGGGCTTCTG
3951  ATTACAAGGT ATCTTGAGAT TCTGGGATCA CATATTCCTT CATCGTACAA
4001  CCTGGAGATG AGATTAGAAT CTTGTGGGAA TTCTCTTGGG TTGTTGTGGT
4051  GTGCTAGACT TAATTACCCA TGAATGATTT TGTCCTCTTG AGAAAATTTC
4101  AATAGCACAT CTATTAGTGT TTTTTATAAT GTAGGATTTT CGTTTCTAAG
4151  TGATTTTTTT TTTTTTTTAA ATTTTTTTGA GATGGAGCTT TTGCTGTTTC
4201  CCAGGCGGGA GTGCAATGGC GCGCTATCTC GGCGCACTGC AGCCTCCATC
4251  TCCTGGGTTC AAGCAGTTCT GCCTCAGCCT CCCGAGTAGC GGGATTACAG
4301  GTGCCCACCA CCACACCCTA CTAATTTTGT ATTTTAGTAG AGACGACATT
4351  TCACCATGTT GGCCAGGCTG GCTCTGAACT TTGACCTCAG GTGATCCACC
4401  CACCTTAGGC TCTCCCAAAG TGCTAGGATT ACAGGTGAGA TATGCTGCGC
4451  CCGGCCCCAA GTGATCTATT CTTGCCATGA CTGTTAACTA AACATGGTGA
4501  CAGGATTCGA TTTTCTTTAC ATTAGATTTG AAAACCGATG TTGGTTTTGG
```

FIGURE 49(5)

4551 GAGATTGCTG CAATTTTTAG GTGACTTCTC TTTCAGACTC TGAAGAAGAA

4601 GCTATGGAGA CTACACCAGC CAAAGGAAAG AAAGCTGCAA AAGTTGTTCC

4651 TGTGAAAGCC AAGAACGTGG CTGAGGATGA AGATGAAGAA GAGGATGATG

4701 AGGACGAGGA TGACGACGAC GACGAAGATG ATGAAGATGA TGATGATGAA

4751 GATGATGAGG AGGAGGAAGA AGAGGAGGAG GAAGGTACTT AAATTAGATT

4801 CTGACATACG ACATGAGTTA TGTTTAAAGG AGGCACTTAA GTGTTTGTGG

4851 CTACTGATGT GTGATACATT GTTTGACATC TTGTCCAGAG CCTGTCAAAG

4901 AAGCACCTGG AAAACGAAAG AAGGAAATGG CCAAACAGAA AGCAGCTCCT

4951 GAAGCCAAGA AACAGAAAGT GGAAGGTAAC TTGCAGAATT AGGGGATATG

5001 GGGGAGATAA ACAGCACAAA TGATGAATAA CAAAGGGACT TAATACTGAA

5051 ACCAGATGTT ACATTGTAGT GTGCTGATGT GCTGTGTATA GAAATTTTGC

5101 TTTGGAAACT AACTTTTTAC CACACTACAA GTAGACTGAG TTGAGCTTTT

5151 TTTGTGCAGG CACAGAACCG ACTACGGCTT TCAATCTCTT TGTTGGAAAC

5201 CTAAACTTTA ACAAATCTGC TCCTGAATTA AAAACTGGTA TCAGCGATGT

5251 TTTTGCTAAA AATGATCTTG CTGTTGTGGA TGTCAGAATT GGTATGACTA

5301 GGTAGCTGCT TCACTGCACG TTACATACCG TGGGTCTGTT AATTTTTCCT

5351 TCCCCTGTTA GCACAGTTAC TTTAGCCTGC CACTGTTAAA CATGAATACT

5401 GTAAACACTT CAAGGTTAGC ATTAGTGAAC TAAGTTAGAA TTAAACTGTA

5451 GATCCCCTAA GTTGCAATTT CCATAATCAG TCGTAACTTG GTATAGCACA

5501 GAATAATTTT TAGTAATTTT TTTGTTGTTT TTGTTATGTA TTGAGACGGA

5551 CGCTGGCTTT TGTTCAGGCT GGAGTACAGT GGCGCAATCT TGGCTCACTG

5601 CAACCTCTGC CTCCCGGGTT CAAGCGATTC TCCTGCCTAA CCTCCCAAGT

5651 GACTGGGATA CGGGTGCCAC TCACCATGCA TGGCTAATTT TTGTTTTGTA

5701 TTTAGTATCG ATTTCACCAT GTTGGTCGGC TGGTTTTGAA CTCCTGACCT

FIGURE 49(6)

```
5751  CAAGTGATCC ACCCACCTCG GCCTCTCGAA GTGCTGGTAC AGCGTCACCA
5801  CCCTGCCAGT AAGTTTTAAT AATTTGGTGT TAGGTGGGAG AATGCTTGAA
5851  CCTGGGAGGC AGAGGTTGCA GTGAGCCAAG TTCGCGCCAC TGTACTCCAG
5901  CCTGGGCAAC AGATTGAGAC ACCGTCTCAA TTTAAAATAA TGTTTATTTT
5951  CTTGGAAGTA CCTTGAAACT ATTAGACCTG TCTAGTCATC ATAGTGAATA
6001  CTTTTATCCA GACAGGATTC TCCTGTATTA GTGCTTATAG GTGTTCTTTT
6051  GTCAGCTGCT ACTGTGAATT CTTATAAGCA ATTTAGCTCC ATGATGAAGA
6101  CCTCAAACGT GAATGTGCAT GTCATATCTT CATGCTGAGC CGTGTTCTGT
6151  AGCTGCAGTT TGCAGAGCCT TGACTTTGTT TTGCTATACT AGGGGTGCTT
6201  TTTAAAATGT GATCTTTGTT TGCACCATCA CATTTGTCTA GATACAGATT
6251  GTGATTTTGA TTTGTGTTTT CACCTGTTGT AATTTTGCCC TCCTCTCCAC
6301  CTGAAGGAAA TTTGGTTATG TGGATTTTGA ATCTGCTGAA GACCTGGAGA
6351  AAGCGTTGGA ACTCACTGGT TTGAAAGTCT TTGGCAATGA AATTAAACTA
6401  GAGAAACCAA AAGGAAAAGA CAGTAAGAAA GGTATGTAAG GCTTTATGAG
6451  TTATGCAATG AACTCAGGAG CTAGACTGCT AGGGAAAATG CTTTGTAACC
6501  CATTTCCCTT TGGTTTCCTC TTATTTTTTT TAAATCATTT TTTTCCTTTG
6551  GTTTCCTCTT AATGTGGGAA TTAAATGAGC TACAGTGTTT ACAAGGTACT
6601  TGGCACTGCT TGTCAGTGTA TAGGTAAATT CCTGAGTTAG GCAAGCAAGA
6651  GCACTCTTAT ACAGAACAAG AACCATTACA TGCACCTAAA TTAAGCTAAG
6701  GATCTTTCTT CACTGAAACT AGTTAGGTCC CTAATTACTC CCTATATACA
6751  GTGTAATGTT TTGAATTGGT ACATTCACTT TTTTTGTTAT GCGCGTCTAC
6801  TCTAGGTTGA ACTCCAGTGT ACCTAACAGA GAGTTTGACA TCAAGGCTGT
6851  GACAACATGG AGGGACCACT TGTGTGTTGA CACTGCTATA TCTCCATATT
6901  TAGCACCGAG CCTTGTACAT ATAGGATCTC AAATTATTTG TTGATAGAGC
6951  TATGTGTGTT TTTCCCCTCT TTTTGTTGTT GCCCCCCACC TTTGGTTTTT
```

FIGURE 49(7)

7001 CAGGCCACAG AGCTCATTTT TGTTTTTTTA ATCTAGAGCG AGATGCGAGA

7051 ACACTTTTGG CTAAAAATCT CCCTTACAAA GTCACTCAGG ATGAATTGAA

7101 AGAAGTGTTT GAAGATGCTG CGGAGATCAG ATTAGTCAGC AAGGATGGGA

7151 AAAGTAAAGG GTATGTTCTT CTATTGAAAT GTAAGGGTTT TATTAACATT

7201 AATGCACTTC CTGCTTTATA AAAGAAATAT TGGTTTGATT TCCTTAGGCG

7251 TGTAACTTGG ACAGTTTAAC CTGTAAGTTT GTGCCTCAGT AACCCATCTG

7301 TACCATGGGG ATAATGTACT CATAGGGTGA TTTTAAAAGA CAAAGCTAAT

7351 ACTTACAAAG AAGCAAGTTT AATGCCTATC TTACATAAAT ACTTTGTAAG

7401 TAGTAGCAGT TCTTTCAGTG AGGTGAGGTT ACATGAAAAA ATTCCAAGTA

7451 TTTGTAAAAC TAGTGGGAAG TAAGAGGGAA GCTCGAGTTT TGATTGAAAA

7501 GTGGACTAAA CAAGGGCATT TTATGTACTC AGATCTGAAG CAAGTTCTGT

7551 GTTGCTGAGG TAAAAGCATT TGTGTTAATA TGGTTTTAAA AACCATGAGT

7601 TCTTCTCCCT CCATTGCAGG ATTGCTTATA TTGAATTTAA GACAGAAGCT

7651 GATGCAGAGA AAACCTTTGA AGAAAAGCAG GGAACAGAGA TCGATGGGCG

7701 ATCTATTTCC CTGTACTATA CTGGAGAGAA AGGTCAAAAT CAAGACTATA

7751 GAGGTGGAAA GAATAGCACT TGGAGTGGTA AGAAATTAGG CTTGTTCCAA

7801 GGTTTTCAGA ATTGGTTGAG GGAACTCTTC TAGTCTTTGT ATTTCATAAG

7851 TTTATAAATA CTTTTTAATC AAAGTTACTC AAATGTAGGT GAAGATCAAG

7901 GACATGATAC CCCAAGTCAT ACTCTTATTT GGAATAGTAA TTTCCAATCT

7951 TGAAATGAGA GCTCTAAATC ATTTTGCATT GGAATACAGT AGGCAAATCA

8001 AGCTTCCTTT GTAGGCATGT TTTATACTTT AAATGACTTG ACCATGTGCG

8051 TTTTGAACTC AGATGATTCT AGGAAAACAG ACCAGTCATC AGCCTATGTA

8101 AGAACAACCA GCAGGACATT GCAACACGTA CTAGGTACTT AATATGTTGA

8151 GTAACAGAAA TGGATTTAGC TTACGTCATG AGTATTTGTA TATAACTCAA

FIGURE 49(8)

8201 GCACTGAAAT TCTTAGGGAA TAGATATTAC TGTTGTGACC GAAGCTGGGA

8251 CACTGTTTCA GAGTCTTAGG AATGTGGCTC TCTATTTCGA GGTGAATCAA

8301 AAACTCTGGT TTTAAGCAAC CTCTCCTACA GTGCAACAGA AGAAACTCTT

8351 CAGGAAGTAT TTGAGAAAGC AACTTTTATC AAAGTACCCC AGAACCAAAA

8401 TGGCAAATCT AAAGGGTAAG ATAATACCTT TGTATCATCA GTTATAGGCC

8451 TATATATGTC TTAGAGGTCT AAGGACGTAA GGTCATGTGT CCTGTAGAAA

8501 AAAGCTAAAT AATTTTAGCC TAGTAAATGA GTGTAAAATA AGTATATTTA

8551 GGTCCAACCT TGAGAGAAGG GCCTTGGCCA GATCATGTGA CCAGTGGTAT

8601 AGAGAGCATG TGCCTGGTAA ATTACTCTAA GCATTAACTG TTCATCCTCA

8651 GGTATGCATT TATAGAGTTT GCTTCATTCG AAGACGCTAA AGAAGCTTTA

8701 AATTCCTGTA ATAAAAGGGA AATTGAGGGC AGAGCAATCA GGCTGGAGTT

8751 GCAAGGACCC AGGGGATCAC CTAATGCCAG AAGCCGTAAG TTCACCTGGT

8801 TAGGGTGCTG TGGTTGGGGG TAGCACTCTC GGTGCTTTGT TTATTTTTGC

8851 ACAAATTCTG TGTTTCCTGT TCGCTACTGA GTGAACAATA ACTGGATATC

8901 GATGACTGAT TACCTGAGAA ATAATTGATG AAATCTCAAG AAAATTCCTC

8951 TAGATAGTCA AGTTCTGATC CAGCTGTCGT CAACTCAGAG TAGCAAGTTT

9001 GCCCATGATT TCCTGCCCCA TCCACTGGGC CCCACCTGCT TGGGTTGCTT

9051 TCCCACTTTC CATAGAAGAC TGGGGCAGGA TATCAACTAT GCAATGGCAA

9101 TTAAAAAATG TAAACCCAGA ATAGCCTTTA CTTTAATTAA GGACTAGTTG

9151 GCTTAGTTGC TTTTAACTGC TTTTTCACTA TAACAAGTAT CTTGGCTAGT

9201 AGTCATACTA GGCATTGTGC AAATTCAGTG TACGAACTGT GAATTCACAT

9251 AAATCGCAAA TTTTTTTTTC CTTCCCAGAG CCATCCAAAA CTCTGTTTGT

9301 CAAAGGCCTG TCTGAGGATA CCACTGAAGA GACATTAAAG GAGTCATTTG

9351 ACGGCTCCGT TCGGGCAAGG ATAGTTACTG ACCGGGAAAC TGGGTCCTCC

9401 AAAGGGTAAG GGAAGGAAGC GTGAGTGCTG CTTCCACTTG AAGGGGTTTT

FIGURE 49(9)

```
 9451  TGTTCTGTGC AGACCTTGAG TCTAATGTGT CTTCTCATTG AGCTCCTTCT
 9501  GTCTATCAGT GGCAGTTTAT GGATTCGCAC GAGAAGAAGA GAGAATTCAC
 9551  AGAACTAGCA TTATTTTACC TTCTGTCTTT ACAGAGGTAT ATTTAGCTGT
 9601  ATTGTGAGAC ATTCTGGGGT TCAAGCTGTC ACACCAGTTA GTTTTCCATA
 9651  GAGAGCTACT CTGCTGCACT GGTATCTTTT TCCCAAATAA ACAAGGCTAC
 9701  TTCTGTGGGA TGGCTCCCCA GCATGTACAG TTAACTTGGG ACATGTGTAG
 9751  TAGGTGCTTT TTATAATGGG CAATTTCATT TGGTGTTCTA GGTTTGGTTT
 9801  TGTAGACTTC AACAGTGAGG AGGATGCCAA GGAGGCCATG GAAGACGGTG
 9851  AAATTGATGG AAATAAAGTT ACCTTGGACT GGGCCAAACC TAAGGGTGAA
 9901  GGTGGCTTCG GGGGTCGTGG TGGAGGCAGA GGCGGCTTTG GAGGACGAGG
 9951  TGGTGGTAGA GGAGGCCGAG GAGGATTTGG TGGCAGAGGC CGGGGAGGCT
10001  TTGGAGGTAA GGCACGCAGA GATAATGACA CCACATAGCA TGTGCTCTTC
10051  AGACCCTGTG CCCTGTCACG GTTCCTAATC ACTGGGGAGG AGGAGCTTTG
10101  TACCCATTCT TTTAACAGTG TCTTGCCTTC CTCCTGTAGG GCGAGGAGGC
10151  TTCCGAGGAG GCAGAGGAGG AGGAGGTGAC CACAAGCCAC AAGGAAAGAA
10201  GACGAAGTTT GAATAGCTTC TGTCCCTCTG CTTTCCCTTT TCCATTTGAA
10251  AGAAAGGACT CTGGGGTTTT TACTGTTACC TGATCAATGA CAGAGCCTTC
10301  TGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT TGGAAATCCG
10351  TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTTGA CTGGATATTC
10401  ATATAAACTT TTTAAAGAGT TGAGTGATAG AGCTAACCCT TATCTGTAAG
10451  TTTTGAATTT ATATTGTTTC ATCCCATGTA CAAAACCATT TTTTCCTACA
10501  AATAGTTTGG GTTTTGTTGT TGTTACTTTT TTTTTTGTTT TTGTTTTTTT
10551  TTTTTTTGCG TTCGTGGGGT TGTAAAAGAA AAGAAAGCAG AATGTTTTAT
10601  CATGGTTTTT GCTTCACCGC TTTAGGACAA ATTAAAAGTC AACTCTGGTG
```

FIGURE 49(10)

```
10651  CCAGACGTGT TACTTCCTAA AGAGTGTTTC CCCTGGAATC TCACTGGAGA

10701  GCATGGCAAA GCCAGCTCTG CCACTTGCTT CACCCATCCC AATGGAAATG

10751  GCTTAGTGCG TGTTTCCAGT ATCCCAGCCC TAACTAACTT GGTTGAAATG

10801  CTGGTGAGGG GACCTGCTCC TGCAGCCCTG GTGCTGACTT GAAGGCTGCT

10851  GCAGCTTCTC CTACTTTTAG CAGGTCTCGA GGATTATGTC TGAAGACCAC

10901  TCTGGAAAGA GGTCGAGGAA CAGATTAGTC AGGTTTCCTA GG
```

FIGURE 49(11)

III.

"MEMGRRIHLELRNRTPSDVKELVLDNSRSNEGKLEGLTDEFEEL
EFLSTINVGLTSIANLPKLNKLKKLELSDNRVSGGLEVLAEKCPNLTHLNLSGNKIKD
LSTIEPLKKLENLKSLDLFNCEVTNLNDYRENVFKLLPQLTYLDGYDRDDKEAPDSDA
EGYVEGLDDEEEDEDEEEYDEDAQVVEDEEDEDEEEEGEEEDVSGEEEEDEEGYNDGE
VDDEEDEEELGEEERGQKRKREPEDEGEDDD"

FIGURE 49(12)

III.

```
   1  GCTGGTTGAG CCTTCAAAGT CCTAAAACGC GCGGCCGTGG GTTCGGGGTT
  51  TATTGATTGA ATTCCGCCGG CGCGGGAGCC TCTGCAGAGA GAGAGCGCGA
 101  GAGATGGAGA TGGGCAGACG GATTCATTTA GAGCTGCGGA ACAGGACGCC
 151  CTCTGATGTG AAAGAACTTG TCCTGGACAA CAGTCGGTCG AATGAAGGCA
 201  AACTCGAAGG CCTCACAGAT GAATTTGAAG AACTGGAATT CTTAAGTACA
 251  ATCAACGTAG GCCTCACCTC AATCGCAAAC TTACCAAAGT TAAACAAACT
 301  TAAGAAGCTT GAACTAAGCG ATAACAGAGT CTCAGGGGGC CTGGAAGTAT
 351  TGGCAGAAAA GTGTCCGAAC CTCACGCATC TAAATTTAAG TGGCAACAAA
 401  ATTAAAGACC TCAGCACAAT AGAGCCACTG AAAAAGTTAG AAAACCTCAA
 451  GAGCTTAGAC CTTTTCAATT GCGAGGTAAC CAACCTGAAC GACTACCGAG
 501  AAAATGTGTT CAAGCTCCTC CCGCAACTCA CATATCTCGA CGGCTATGAC
 551  CGGGACGACA AGGAGGCCCC TGACTCGGAT GCTGAGGGCT ACGTGGAGGG
 601  CCTGGATGAT GAGGAGGAGG ATGAGGATGA GGAGGAGTAT GATGAAGATG
 651  CTCAGGTAGT GGAAGACGAG GAGGACGAGG ATGAGGAGGA GGAAGGTGAA
 701  GAGGAGGACG TGAGTGGAGA GGAGGAGGAG GATGAAGAAG GTTATAACGA
 751  TGGAGAGGTA GATGACGAGG AAGATGAAGA AGAGCTTGGT GAAGAAGAAA
 801  GGGGTCAGAA GCGAAAACGA GAACCTGAAG ATGAGGGAGA AGATGATGAC
 851  TAAGTGGAAT AACCTATTTT GAAAAATTCC TATTGTGATT TGACTGTTTT
 901  TACCCATATC CCCTCT
```

FIGURE 49(13)

IV.

"MSAPAAKVSKKELNSNHDGADETSEKEQQEAIEHIDEVQNEIDR
LNEQASEEILKVEQKYNKLRQPFFQKRSELIAKIPNFWVTTFVNHPQVSALLGEEDEE
ALHYLTRVEVTEFEDIKSGYRIDFYFDENPYFENKVLSKEFHLNESGDPSSKSTEIKW
KSGKDLTKRSSQTQNKASRKRQHEEPESFFTWFTDHSDAGADELGEVIKDDIWPNPLQ
YYLVPDMDDEEGEGEEDDDDDEEEEGLEDIDEEGDEDEGEEDEDDDEGEEGEEDEGED
D"

IV.

```
   1  CGACCGCGGA GCAGCACCAT GTCGGCGCCG GCGGCCAAAG TCAGTAAAAA
  51  GGAGCTCAAC TCCAACCACG ACGGGGCCGA CGAGACCTCA GAAAAAGAAC
 101  AGCAAGAAGC GATTGAACAC ATTGATGAAG TACAAAATGA AATAGACAGA
 151  CTTAATGAAC AAGCCAGTGA GGAGATTTTG AAAGTAGAAC AGAAATATAA
 201  CAAACTCCGC CAACCATTTT TTCAGAAGAG GTCAGAATTG ATCGCCAAAA
 251  TCCCAAATTT TTGGGTAACA ACATTTGTCA ACCATCCACA AGTGTCTGCA
 301  CTGCTTGGGG AGGAAGATGA AGAGGCACTG CATTATTTGA CCAGAGTTGA
 351  AGTGACAGAA TTTGAAGATA TTAAATCAGG TTACAGAATA GATTTTTATT
 401  TTGATGAAAA TCCTTACTTT GAAAATAAAG TTCTCTCCAA AGAATTTCAT
 451  CTGAATGAGA GTGGTGATCC ATCTTCGAAG TCCACCGAAA TCAAATGGAA
 501  ATCTGGAAAG GATTTGACGA AACGTTCGAG TCAAACGCAG AATAAAGCCA
 551  GCAGGAAGAG GCAGCATGAG GAACCAGAGA GCTTCTTTAC CTGGTTTACT
 601  GACCATTCTG ATGCAGGTGC TGATGAGTTA GGAGAGGTCA TCAAAGATGA
 651  TATTTGGCCA AACCCATTAC AGTACTACTT GGTTCCCGAT ATGGATGATG
 701  AAGAAGGAGA AGGAGAAGAA GATGATGATG ATGATGAAGA GGAGGAAGGA
 751  TTAGAAGATA TTGACGAAGA AGGGGATGAG GATGAAGGTG AAGAAGATGA
 801  AGATGATGAT GAAGGGGAGG AAGGAGAGGA GGATGAAGGA GAAGATGACT
 851  AAATAGAACA CTGATGGATT CCAACCTTCC TTTTTTTAAA TTTTCTCCAG
 901  TCCCTGGGAG CAAGTTGCAG TCTT
```

V.

CTTCGGGTGTACGTGCTCCGGGATCTTCAGCACCCGCGGCCGCCATCGCCGTCGCTTGGCTTCTTCTGGACTCATCTGCG
CCACTTGTCCGCTTCACACTCCGCCGCCATCATGGTGAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGACCCCAAGAAAA
TGGCTCCTCCTCCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAATGTCAGAAGATGAAGAAGATGATAGCAGTGGA
GAAGAGGTCGTCATACCTCAGAAGAAAGGCAAGAAGGCTGCTGCAACCTCAGCAAAGAAGGTGGTCGTTTCCCCAACAAA
AAAGGTTGCAGTTGCCACACCAGCCAAGAAAGCAGCTGTCACTCCAGGCAAAAAGGCAGCAGCAACACCTGCCAAGAAGA
CAGTTACACCAGCCAAAGCAGTTACCACACCTGGCAAGAAGGGAGCCACACCAGGCAAAGCATTGGTAGCAACTCCTGGT
AAGAAGGGTGCTGCCATCCCAGCCAAGGGGGCAAAGAATGGCAAGAATGCCAAGAAGGAAGACAGTGATGAAGAGGAGGA
TGATGACAGTGAGGAGGATGAGGAGGATGACGAGGACGAGGATGAGGATGAAGATGAAATTGAACCAGCAGCGATGAAAG
CAGCAGCTGCTGCCCCTGCCTCAGAGGATGAGGACGATGAGGATGACGAAGATGATGAGGATGACGATGACGATGAGGAA
GATGACTCTGAAGAAGAAGCTATGGAGACTACACCAGCCAAAGGAAAGAAAGCTGCAAAAGTTGTTCCTGTGAAAGCCAA
GAACGTGGCTGAGGATGAAGATGAAGAAGAGGATGATGAGGACGAGGATGACGACGACGACGAAGATGATGAAGATGATG
ATGATGAAGATGATGAGGAGGAGGAAGAAGAGGAGGAGGAAGAGCCTGTCAAAGAAGCACCTGGAAAACGAAAGAAGGAA
ATGGCCAAACAGAAAGCAGCTCCTGAAGCCAAGAAACAGAAAGTGGAAGGCACAGAACCGACTACGGCTTTCAATCTCTT
TGTTGGAAACCTAAACTTTAACAAATCTGCTCCTGAATTAAAAACTGGTATCAGCGATGTTTTTGCTAAAAATGATCTTG
CTGTTGTGGATGTCAGAATTGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAAGACCTGGAGAAAGCG
TTGGAACTCACTGGTTTGAAAGTCTTTGGCAATGAAATTAAACTAGAGAAACCAAAAGGAAAAGACAGTAAGAAAGAGCG
AGATGCGAGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAATTGAAAGAAGTGTTTGAAGATGCTG
CGGAGATCAGATTAGTCAGCAAGGATGGGAAAAGTAAAGGGATTGCTTATATTGAATTTAAGACAGAAGCTGATGCAGAG
AAAACCTTTGAAGAAAAGCAGGGAACAGAGATCGATGGGCGATCTATTTCCCTGTACTATACTGGAGAGAAAGGTCAAAA
TCAAGACTATAGAGGTGGAAAGAATAGCACTTGGAGTGGTGAATCAAAAACTCTGGTTTTAAGCAACCTCTCCTACAGTG
CAACAGAAGAAACTCTTCAGGAAGTATTTGAGAAAGCAACTTTTATCAAAGTACCCCAGAACCAAAATGGCAAATCTAAA
GGGTATGCATTTATAGAGTTTGCTTCATTCGAAGACGCTAAAGAAGCTTTAAATTCCTGTAATAAAAGGGAAATTGAGGG
CAGAGCAATCAGGCTGGAGTTGCAAGGACCCAGGGGATCACCTAATGCCAGAAGCCAGCCATCCAAAACTCTGTTTGTCA
AAGGCCTGTCTGAGGATACCACTGAAGAGACATTAAAGGAGTCATTTGACGGCTCCGTTCGGGCAAGGATAGTTACTGAC
CGGGAAACTGGGTCCTCCAAAGGGTTTGGTTTTGTAGACTTCAACAGTGAGGAGGATGCCAAGGAGGCCATGGAAGACGG
TGAAATTGATGGAAATAAAGTTACCTTGGACTGGGCCAAACCTAAGGGTGAAGGTGGCTTCGGGGGTCGTGGTGGAGGCA
GAGGCGGCTTTGGAGGACGAGGTGGTGGTAGAGGAGGCCGAGGAGGATTTGGTGGCAGAGGCCGGGGAGGCTTTGGAGGG
CGAGGAGGCTTCCGAGGAGGCAGAGGAGGAGGAGGTGACCACAAGCCACAAGGAAAGAAGACGAAGTTTGAATAGCTTCT
GTCCCTCTGCTTTCCCTTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTTACTGTTACCTGATCAATGACAGAGCCTTCT
GAGGACATTCCAAGACAGTATACAGTCCTGTGGTCTCCTTGGAAATCCGTCTAGTTAACATTTCAAGGGCAATACCGTGT
TGGTTTTGACTGGATATTCATATAAACTTTTTAAAGAGTTGAGTGATAGAGCTAACCCTTATCTGTAAGTTTTGAATTTA
TATTGTTTCATCCCATGTACAAAACCATTTTTTCCTAC

FIGURE 49(14)